







CC glutamatergic ligands. Its amino acid sequence was determined from  
CC cDNA clones (see also T38322) obt'd. from a human retinal cDNA library.  
CC A splice variant has an alternative N-terminal sequence (see also  
CC W01100). Recombinant receptors, practically free of contamination  
CC by other receptors, can be produced in host cells. The receptors,  
CC and cells expressing them, are used in drug screening to identify  
SQ cpds. that modulate mGluR6.  
Sequence 877 AA;

Query Match 3.3%; Score 225; DB 1; Length 877;  
Best Local Similarity 21.5%; Pred. No. 5,82e-07;  
Matches 60; Conservative 91; Mismatches 106; Indels 22; Gaps 19;

Db 592 LAVGIATTTVAATVRYNNDPIVRSAGRELSVLLTGIFLYA-I-TF-L--WVAP 645  
Y 487 LTIIGIMASAFLEFN-KNNOKLIKSSPYNNLLIIGMLSYASIFLFGDGSVSEK 546  
Db 646 G-AAVCAARLEFLGGLTISYSLTKNTIYIFEOGKRSVTPPPFISQVITFSL 704  
Y 547 TFEITLCTVRITWLTGVTATFAGMAFKATWVHAIFKNVK--MKKK-IIRDOKLVIYVGM 603  
Db 705 TSIQVGMIMLGAAPPHSYID-YE-EQRTVDEPA-RGYLK-CDMSDSL-IGCL-GY- 757  
Y 604 LLLDCLILICWQAVDPRLRTVERYSMEPPDAGDISIRPLEHCENTHMTWIGIYAYK 663  
Db 758 SLLIMVTC-TVAIKRGVPEFNEAKPIGFMTTCIIMLAFPIPFCTAQAERKIYIO 816  
Y 664 GLMLTFGCFIAMETRVNSIP-ALNDSKIYIGMSYNNVICIIGAAVSFLTRQPNVQFC- 721  
Db 817 TITLTVSLSASVSLGMLYPRVYIILFHPEQNVOKRK 855  
Y 722 IVALVI-I-FCSTITLCLVFPKLTILTPNDAQTNR 758

RESULT 8  
ID W49928 standard; Protein; 908 AA.  
AC W49928;  
DT 09-JUN-1998 (first entry)  
DE Human metabotropic glutamate receptor (mGluR).  
KW Metabotropic glutamate receptor; mGluR; screening; stroke; epilepsy;  
KW Alzheimer's disease; Parkinson's disease; Huntington's disease.  
OS Homo sapiens.  
PN W09748724-R2.  
PD 24-DEC-1997.  
PE 20-FEB-1997; U09025.  
PR 21-FEB-1996; US-604298.  
PA (NPSF-) NPS PHARM INC.  
PI Fuller FH, Hammerland LG, Simin RT, Stormann TM.  
DR WPI: 98-063076/06.  
N-PSDB: V17116.  
PT Novel human metabotropic glutamate receptor - for screening  
PT compounds useful for treating e.g. stroke, epilepsy or diseases such  
PT as Alzheimer's, Parkinson's or Huntington's diseases  
PS Claim 7; Fig 1; 98pp; English.  
CC This is a novel human metabotropic glutamate receptor (mGluR). A  
CC purified or isolated nucleic acid of at least 15 nucleotides in length  
CC encoding at least 6 contiguous amino acids of the unique portion of this  
CC mGluR can be used to generate transgenic mammals by insertion of the  
CC nucleic acid into the mammalian genome. The mGluR can be used to screen  
CC for compounds which modulate its activity, especially in the  
CC physiological functions of convulsions, neuroprotection, neuronal death  
CC and development, central control of cardiac activity, waking, control of  
CC movement and control of vestibulo-ocular reflex. Such compounds can be used  
CC to treat glutamate excitotoxicity, global and focal ischaemic and  
CC haemorrhagic stroke, head trauma, spinal cord injury, hypoxia-induced  
CC nerve damage, epilepsy or neurodegenerative diseases such as Alzheimer's,  
CC Parkinson's or Huntington's diseases.  
SQ Sequence 908 AA;

Query Match 3.3%; Score 231; DB 1; Length 908;  
Best Local Similarity 21.9%; Pred. No. 2.12e-07;  
Matches 62; Conservative 97; Mismatches 100; Indels 24; Gaps 21;

Db 590 VALIGII-ATTEVIVATVRYNNDPIVRSAGRELSVLLTGIFLCYSITFLM-I-AA--PD 644  
Y 487 LTIIGIMASAFLEFN-IKNNOOLIKSSPYNNLLIIGMLSYASIFLFGDGSVSE 545  
Db 645 -TI--ICFRRVFLGGLGCSYALTKNTIYIFEOGKRSVTPAPFISQVITFSS 701  
Y 546 KTFEITLCTVRITWLTGVTATFAGMAFKATWVHAIFKNVK-K--KIRDOKLVIYVG 602  
Db 702 LISVOLLGVFVWVDPPIIID-YG-EQRTLDEKA-RGYLK-CDISDSL-IGSL-GY 755  
Y 603 MLLDCLILICWQAVDPRLRTVERYSMEPPDAGDISIRPLEHCENTHMTWIGIYAY 662  
Db 756 SLLIMV-TC-TVAIKRGVPEFNEAKPIGFMTTCIIMLAFPIPFCTAQAERKIY 813  
Y 663 KGLMLTFGCFIAMETRVNSIP-ALNDSKIYIGMSYNNVICIIGAAVSFLTRQPNVQFC 721  
Db 814 OTTILTVMSLSASVSLGMLYPRVYIILFHPEQNVOKRRSF 856  
Y 722 -IVALVI-I-FCSTITLCLVFPKLTILTPNDAQTNR 761

RESULT 9  
ID R82658 standard; Protein; 912 AA.  
AC R82658;  
DT 20-DEC-1995 (first entry)  
DE Human mGluR4.  
KW Metabotropic glutamate receptor 4; mGluR4; stroke; epilepsy;  
KW Alzheimer disease; detection; diagnosis; therapy.  
OS Homo sapiens.  
FH Key  
FT Location/Qualifiers  
FT domain  
FT /label= TMD-I  
FT /note= "Transmembrane domain I"  
FT 625..645  
FT /label= TMD-II  
FT /note= "Transmembrane domain II"  
FT 657..675  
FT /label= TMD-III  
FT /note= "Transmembrane domain III"  
FT 699..720  
FT /label= TMD-IV  
FT /note= "Transmembrane domain IV"  
FT 751..771  
FT /label= TMD-V  
FT /note= "Transmembrane domain V"  
FT 786..807  
FT /label= TMD-VI  
FT /note= "Transmembrane domain VI"  
FT 823..847  
FT /label= TMD-VII  
FT /note= "Transmembrane domain VII"  
PN W09522609-A2.  
PD 24-AUG-1995.  
PE 21-FEB-1995; G00356.  
PR 21-FEB-1994; GB-003285.  
PR 01-AUG-1994; GB-015532.  
PA (WELL) WELLCOME FOUND LTD.  
PI Makoff AJ.  
DR WPI: 95-302715/39.  
N-PSDB: T03888.  
PT New isolated human metabotropic glutamate receptors - used for  
PT detection, diagnosis and therapy of diseases associated with the  
PT receptors, eg. stroke, epilepsy and Alzheimer's disease.  
PS Claim 2; Page 40-43; 55pp; English.  
CC mRNA from the human cerebellum was used to construct a cDNA  
CC library. cDNA was amplified by PCR primers (T03896-97) based on rat  
CC mGluR4 sequences and with the primers given in T03898-99 to obtain  
CC cDNA encoding human mGluR4.  
SQ Sequence 912 AA;

Query Match 3.3%; Score 228; DB 1; Length 912;  
Best Local Similarity 21.6%; Pred. No. 3.51e-07;  
Matches 62; Conservative 98; Mismatches 100; Indels 27; Gaps 22;





Query Match	24.3%;	Score 1680;	DB 1;	Length 844;
Best Local Similarity	35.1%;	Pred. No. 4.32e-126;		
Matches 262;	Conservative 192;	Mismatches 269;	Indels 23;	Gaps 21;

RESULT	4
ID	W40116 standard; Protein; 960 AA.
AC	W40116;
DT	03-JUN-1998 (first entry)

Query Match	24.2%;	Score 1672;	DB 1;	Length 960;
Best Local Similarity	36.0%;	Pred. No. 2.04e-125;		
Matches	248;	Conservative 177;	Mismatches 247;	Indels 16; Gaps 14;

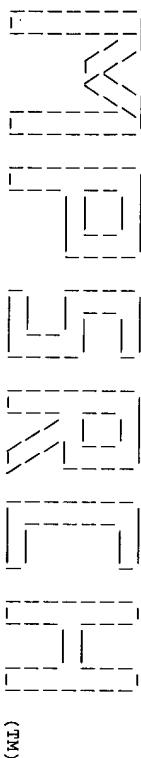
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Db 184 GQACQAPVAAEADENSRDILPQTEKLHHSCDQPGAKRYKLYELLNDPIKILMP 243
Qy 73 GRGLVPVLAELQIRNE-SLIRPFJDLRLYDECNAGLKAFLDAKTKGPNHLMFG 131
Db 244 G-CSVSUVALEAARMNLIVSYGSSSPALSNOREFPFRRHPSPATLHNTPKLEK 302
Qy 132 GVCPSVTSIAESLQGNLYQJSAFTPLVLAOKKPYFRFRVPBDNANVNAIILK 191
Db 303 WKKKATIQOTTEVFSTLDDLERYEKAGELTFERQSFSDPAVPVKNLRODARIV 362
Qy 192 FMRMRGTLVODORSEVRNDLGVYGEDIEDSTDESNDCPSYKAKLGNVRIIL 251
Db 363 GLPEERARVCEYKKEFEKRYWFLGVAADMF-KTY-DP-SINCYEEMTEAVE 419
Qy 252 GQPDNMAKAVFCFAFEBSKQWITIPQWTEPRAMQCVHEANSSCLRRSLAAME 311
Db 420 GHITTELYMLNPANTRSSIMNTSOFEVEKLRKLRRHPEGTGFQDAPLAVDAIUALA 479
Qy 312 GYGVDEPRLSSQIKITISGRPOQY-ERENS-KRSQGVSPSFH-G-YAYDGIIVAKT 367
Db 480 LNKTSQG--GGRSGVRLDEPNYNNQITDQIYRAMSSFEQVSGHVAFDASGSMATL 537
Qy 368 LQRMATELHASSHROLDQFNTDHTLTKILINMANETNEFFYQGVAF-RNGEEMGTIK 426
Db 538 IEOLGQSYKIKGYVDSFKDLSM-SKDKMGQSPADQITVIKFRFLSOIKFLISV 596
Qy 427 FTYQPDREYKGEVIAADTEIINDTIRQGESEPKDXTIILEOKRISLPLSTLSA 486
Db 597 LSLSGIVLAVVCSFENYNSHVRYIONSOPRLNLTAVGSLAALVAPPLGIDGHIERS 656
Qy 487 LTLIGMIMSASFLEFNKRNQKLLKMSPPMNNLLILGSMLSYABILFLGLDGSFVSE 546
Db 657 QPPLVCARLMLLIGFSIGSGSMFTKIMVYHVIYFKKEKKEKMRKTEPKMLATVGLL 716
Qy 547 TFEFLICVPRWILVGYTAFGAMAKTWYHAIF--KNYKMK-KKIIDOKLIVYGM 603
Db 717 VGMQVYLLAIWQIVPRLHRTETFEKKEPKDDIVSLPOLDESSKKMMNMLGYFYK 776
Qy 604 LLLDCLILIQMAVDRKRYERYSMEDPAGROISIRPLRLCEHTAHTIWLGIYAVIK 663

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QY 161 VLADKKKPYFFERTVSDNANVPAIKLKLHFWRRVGLITDQVQRSEVRNDLIGVLYG 220  
 DB 216 AGIEITRFQSFSDPAVPANLKRQDARIIVGLFEYEAKRYCEVYKRELGKKYVFL 275  
 QY 221 EDIEISTEFSFSDPCSVAKKLGNVRIITLGGFDONMAKAVCCAFESMESKQWII 280  
 DB 276 IGWYADNMF-KIY-DP-SINCTVDEMTAEVGHITTEIYMLNPANTRSISNMTSQEVEK 332  
 QY 281 PGWEPAWMEQVHVEANSRCLRRSLAAAMEGYIGVDFEPLSSKQIKTISGKTPQY-ER 339  
 DB 333 LTRLRKHPEETGGFOAPALAYADAINALALAKTSGG--GGRSGVRLDEPNNTI 390  
 QY 340 EYNS-KRSGVGPSKFEH-G-YAYDGIWIAKTLQRAETLHASSRHQRIQDFNTDHLCK 396  
 DB 391 QIYRAMSSFEQVSGHVFDASGSRMAWTLIELOGSGYKKGYYDSTKDLNW-SKTD 449  
 QY 397 IILNANMETNFGVLTGVVF-RNGERMGTIKFTQFODSREVKAGEVNAVDLEIINDI 455  
 DB 450 KWIIGSPADQTLVITKFRFLSOKLFISVSLGIVLAVVCLSFNINSHVRIQNSQ 509  
 QY 456 RFQSGSEPPKDKTIIIEOLRKISLPLYSILSALTILGIMASAFLEFNKRNOKLIKMS 515  
 DB 510 PNLNLTAVGCSLALAVPLGLDGYHIGNPFVGOARLWTLIGFSLGYSMTFKIM 569  
 QY 516 PYMNNLTILGMSYASIFLGLDGSFVSEKTEETCTVTRTWILVGYTTAFGAKTW 575  
 DB 570 WHTVETFKKEKKEMRKLTLEPKLYATVGLVGMVDTLAIMQIVDPILARTIETFAKEEP 629  
 QY 576 RVHAIIF--KNVKKM-KKIINDQKLVIYGMMLDLCILCQWAVDPLRRTVRYSMEDP 632  
 DB 630 KEDIVSILPOLHEGSSRRKMTWLGIFYGKGLLLIGIFLAYETKSVSTEKINDHRANG 689  
 QY 633 PAGRDISIRPLEHCENTHMTIMGIYVAYKGLMLFGCLAMETRVNSIPALNDSXYIG 692  
 DB 690 MAIYNVAVLICITRPVMTLLSSQODAAFAFASALIAVSSYITLVLPVKMRRLITRGE 748  
 QY 693 MSYVNGIMCITIGAASVFLTRDPNVOCIALVITIFCSTITLCVLFVPRKLITLRTNPD 751  
 RESULT 2  
 ID W40117 standard: Protein: 793 AA.  
 AC W40117;  
 DT 03-JUN-1998 (first entry)  
 DE Human GABA-BR1a/D receptor protein.  
 KW Gamma-aminobutyric acid; GABA-BR1a/D receptor; human; brain; agonist;  
 KW inhibitory neurotransmitter; peripheral nervous system; antagonist;  
 KW treatment; dementia; depression; anxiety; bronchial inflammation; asthma;  
 KW epilepsy; cognitive function.  
 OS Homo sapiens.  
 PN M09746675-A1.  
 PD 11-DEC-1997.  
 PF 19-MAR-1997: E01370.  
 PR 22-NOV-1996: US-756091.  
 PR 30-MAY-1996: US-655716.  
 PA (NOVS ) NOVARTIS AG.  
 PI Bettler B, Bittiger H, Froestl W, Kaupmann K, Mickel SJ;  
 DR N-PSDB: V10265.  
 PT Purified GABA-B receptor or receptor protein - and antagonists of  
 PT these which may be useful in treating nervous system disorders  
 PS Claim 4; Page 62-67; 108pp; English.  
 CC This sequence represents a novel human GABA-B receptor protein,  
 CC GABA-BR1a/D. GABA (gamma-aminobutyric acid) is the major inhibitory  
 CC neurotransmitter found in the brain and peripheral nervous system  
 CC and this receptor may be used for the identification of GABA-B  
 CC receptor agonists and antagonists. Such proteins may be used in  
 CC treatment of dementia, depression, anxiety, epilepsy, spasticity,  
 CC bronchial inflammation or asthma or to improve cognitive function.  
 CC GABA-B receptor ligands and probes derived from this sequence can be  
 CC used to assay for GABA-B receptors or DNA encoding them.  
 DR N-PSDB: V10266.  
 DR Sequence 793 AA;  
 Query Match 24.3%; Score 1676; DB 1; Length 793;

Best Local Similarity 36.0%; Pred. No. 9,386-126;  
 Matches 248; Conservative 179; Mismatches 245; Indels 16; Gaps 14;  
 DB 17 GOACPAVEMALEVNSRDLIPDYELKLHHDSKCPGQATYLYELLYNDPIKILMP 76  
 QY 73 GRGVLPVELAIEQIRNE-SILRREYFLDLRLYDTECNAGLAFYAIKYGNHMLAVFG 131  
 DB 77 G-CSSVSTLVAEARMMNLIVLSYSSSPALSNRQRPETFEFRTHPSATLHPRVKLEEK 135  
 QY 132 GVCPSVTIIESLOGMVLVOLSFPAATPVADKKKPYFFERVPVSDNANVPAIKLK 191  
 DB 136 MGWKIATIQOTTEVFTSLDDEERKREAGIETTFQSFSDPAVPANLKRQDARIIV 195  
 QY 192 FRWRVGTITDQVQFSEVRNDLIGVLTGEDIETSDTESNDCTSVKRLKGNVRIIL 251  
 DB 196 GLFEYTEARKYFCCEYKRELGKKYVFLIGWYADNMF-KIY-DP-SINCTVDEMTAEV 252  
 QY 252 GQFQONMAAKYFCCAFESMSGSKYQWIIIPWYEPAMWQVHYVANSRCLRRSLAAE 311  
 DB 253 GHITTEIYMLNPANTRSISNMTSQEVEKLTRLKRHPETGGFOAPLAYDAIWAALA 312  
 QY 312 GYIGVDFEPLSSKQIKTISGKTPQY-EREYNS-KRSGVGPSKFEH-G-YAYDGIWIAKT 367  
 DB 313 LNKTSGG--GGRSGVRLDEPNNTIITDQIYRAMSSFEQVSGHVFPDASGSRMAWTL 370  
 QY 368 LQRAETLHASSRHQRIQDFNTDHLCKIILNANMETNFGVLTGVVF-RNGERMGTIK 426  
 DB 371 IELOGSGYKKGYYDSTKDLNW-SKTDKWIIGSPADQTLVITKFRFLSOKLFISV 429  
 QY 427 FTQFODSREVKAGEVNAVDLEIINDIRFQSGSEPPKDKTIIIEOLRKISLPLYSILSA 486  
 DB 430 ISSIGIVLAVVCLSFNINSHVRIQNSQPNLNLJAVGSLALAAVPLGLDGYHIGRN 489  
 QY 487 LITLIMASAFLEFNINRNOKLIKMSPPYNNLTILGMLYASIFLGLDGSFVSEK 546  
 DB 490 OFPVCQARMLTLGIFSLGYSMTFKIMWHTVETFKKEKKEMRKLTLEPKLYATVGL 549  
 QY 547 TETCTVTRTWILVGYTTAFGAMFAKTWRVHALF--KNVKKM-KKIINDQKLVIYGM 603  
 DB 550 VGMVDTLAIMQIVDPILARTIETFAKEEPKEDIVSILPOLHEGSSRRKMTWLGIFYGK 609  
 QY 604 LLDLCILCQWAVDPLRKYERYSMEDPAGRDISIRPLEHCENHMTIMGIYVAYK 663  
 DB 610 GLLILGIFLAYETKSVSTEKINDHRANGMAIYNVAVLICITRPVMTLLSSQODAAFA 669  
 QY 664 GLIMFGCLAMETRVNSIPALNDSKYGVNIGICIGAASVFLTRDPNVOCIALV 723  
 DB 670 SLATVFSYITLVLPVKMRRLITRGE 697  
 QY 724 ALVITIFCSTITLCVLFVPRKLITLRTNPD 751  
 RESULT 3  
 ID W40118 standard: Protein: 844 AA.  
 AC W40118;  
 DT 03-JUN-1998 (first entry)  
 DE Rat GABA-BR1b receptor protein.  
 KW Gamma-aminobutyric acid; GABA-BR1b receptor; rat; brain; agonist;  
 KW inhibitory neurotransmitter; peripheral nervous system; antagonist;  
 KW treatment; dementia; depression; anxiety; bronchial inflammation; asthma;  
 KW epilepsy; cognitive function.  
 OS Rattus norvegicus.  
 PN M09746675-A1.  
 PD 11-DEC-1997.  
 PF 19-MAR-1997: E01370.  
 PR 22-NOV-1996: US-756091.  
 PR 30-MAY-1996: US-655716.  
 PA (NOVS ) NOVARTIS AG.  
 PI Bettler B, Bittiger H, Froestl W, Kaupmann K, Mickel SJ;  
 DR N-PSDB: V10266.  
 DR Purified GABA-B receptor or receptor protein - and antagonists of  
 PT these which may be useful in treating nervous system disorders



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Mpsrch\_dp protein - protein database search, using Smith-Waterman algorithm  
Run on: Wed Mar 15 21:49:17 2000; Maspar time 32.56 Seconds  
Tabular output not generated. 683.720 Million cell updates/sec

Title: >US-09-211-755-4  
Description: (1-940) from US09211755.pep  
Perfect Score: 6906  
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Scoring table:  
PAM 150  
Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-geneseq36  
1:geneseqp

Statistics: Mean 39.909; Variance 201.597; scale 0.198

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1684	24.4	844	1 W40119	Human GABA-BR1b recept	1,99e-126
2	1676	24.3	793	1 W40117	Human GABA-BR1a/b rece	9,38e-126
3	1680	24.3	844	1 W40118	Rat GABA-BR1b receptor	4,32e-126
4	1672	24.2	960	1 W40116	Rat GABA-BR1a receptor	2,04e-125
5	267	3.9	38	1 Y13091	Human secreted protein	4,52e-10
6	232	3.4	908	1 W41368	Human metabotropic glu	1,79e-07
7	225	3.3	877	1 W01099	Metabotropic glutamate	5,82e-07
8	231	3.3	908	1 W49928	Human metabotropic glu	2,12e-07
9	228	3.3	912	1 R82658	Human mglur4	3,51e-07
10	228	3.3	912	1 R72092	Human mglur7	3,67e-06
11	214	3.1	867	1 R72093	Human mglur7 clone cmr	3,67e-06
12	214	3.1	867	1 R72093	Human mglur7 clone cmr	3,67e-06
13	217	3.1	915	1 R72097	Human mglur7a	2,22e-06
14	214	3.1	915	1 R80479	Rat metabotropic gluta	3,67e-06
15	214	3.1	922	1 R72098	Human mglur7b	3,67e-06
16	204	3.0	1026	1 W32059	Dogfish shark kidney c	1,93e-05
17	199	2.9	1079	1 W38275	Rat kidney cell calculi	4,39e-05
18	199	2.9	1079	1 W38275	Rat kidney extracellular	4,39e-05
19	199	2.9	1079	1 W54847	Rat kidney calcium rec	4,39e-05
20	199	2.9	1079	1 W89567	Rat parathyroid calculi	4,39e-05
21	193	2.8	872	1 R89560	Metabotropic glutamate	1,17e-04
22	194	2.8	1078	1 W89565	Human parathyroid calc	9,95e-05
23	194	2.8	1078	1 W11869	Parathyroid calcium re	9,95e-05

24	194	2.8	1078	1 W54846	Human parathyroid calc	9,95e-05
25	194	2.8	1078	1 W38274	Human parathyroid cell	9,95e-05
26	192	2.8	1085	1 W38272	Bovine parathyroid cell	1,38e-04
27	192	2.8	1085	1 W54844	Bovine parathyroid cal	1,38e-04
28	192	2.8	1085	1 W89563	Bovine parathyroid cal	1,38e-04
29	194	2.8	1088	1 W89564	Human parathyroid calc	9,95e-05
30	194	2.8	1088	1 W11888	Parathyroid calcium re	9,95e-05
31	194	2.8	1088	1 W38273	Human parathyroid cell	9,95e-05
32	194	2.8	1088	1 W54845	Human parathyroid calc	9,95e-05
33	194	2.8	1219	1 W25763	Amino acid sequence of	9,95e-05
34	184	2.7	872	1 R5052	Human metabotropic glu	5,06e-04
35	188	2.7	877	1 R82657	Human mglur3	2,65e-04
36	188	2.7	879	1 R64252	Human mglur3	5,06e-04
37	184	2.7	1180	1 R64253	Human mglur5a	5,06e-04
38	184	2.7	1212	1 R64254	Human mglur5b	5,06e-04
39	181	2.6	779	1 W94921	Rat pheromone receptor	8,21e-04
40	178	2.6	906	1 R64250	Human mglur1b	1,33e-03
41	178	2.6	906	1 R25081	GLU-G-R subtype 1b	1,33e-03
42	178	2.6	1056	1 W25765	Amino acid sequence of	1,33e-03
43	178	2.6	1056	1 W25764	Amino acid sequence of	1,33e-03
44	178	2.6	1058	1 W25762	Amino acid sequence of	1,33e-03
45	178	2.6	1199	1 R25080	GLU-G-R subtype 1a	1,33e-03

ALIGNMENTS

RESULT 1	ID	W40119	standard; Protein; 844 AA.
AC	W40119	1998 (first entry)	
DT	03-JUN-1998		
DE	Human GABA-BR1b receptor protein.		
KW	Gamma-aminobutyric acid; GABA-BR1a/b receptor; human; brain; agonist;		
KW	Inhibitory neurotransmitter; peripheral nervous system; antagonist;		
KW	treatment; dementia; depression; anxiety; bronchial inflammation; asthma;		
KW	epilepsy; cognitive function.		
OS	Homo sapiens.		
PN	W09746675-A1.		
PD	11-DEC-1997.		
PF	19-MAR-1997; E01370.		
PR	22-NOV-1996; US-756091.		
PR	30-MAY-1996; US-655716.		
PA	(NOVS) NOVARTIS AG.		
PI	Bettler B, Bitliger H, Froestl W, Kaupmann K, Mickel SJ.		
DR	WPI; 98-042183/04.		
DR	N-PSDB; V10267.		
PT	Purified GABA-B receptor or receptor protein - and antagonists of		
PT	these which may be useful in treating nervous system disorders		
PS	Claim 4; Page 86-90; 108pp; English.		
CC	This sequence represents a novel human GABA-B receptor protein,		
CC	GABA-BR1b. GABA (gamma-aminobutyric acid) is the major inhibitory		
CC	neurotransmitter found in the brain and peripheral nervous system		
CC	and this receptor may be used for the identification of GABA-B		
CC	receptor agonists and antagonists. Such proteins may be used in		
CC	treatment of dementia, depression, anxiety, epilepsy, spasticity,		
CC	bronchial inflammation or asthma or to improve cognitive function.		
CC	GABA-B receptor ligands and probes derived from this sequence can be		
CC	used to assay for GABA-B receptors or DNA encoding them.		
SO	Sequence 844 AA;		

Query Match 24.4%; Score 1684; DB 1; Length 844;  
Best Local Similarity 35.3%; Pred. No. 1,99e-126;  
Matches 254; Conservative 191; Mismatches 255; Indels 19; Gaps 17;

Db	40	SRVPPSSERRRAYVIGALFPMK-G-GMPG-GQACQAVALEMDVSRDILPDIYKLK 96
Oy	42	TRGAPRPPSSPUSLIGLMLPTKEVAKSGRGVLAVALAIQINNE-SLRPFYIDL 100
Db	97	IHDSPKDCQATKYIELLYNDPIKIIIMP-G-SSYSTVAEARMMNTIVSYGSSP 155
Oy	101	RLYDECDNAGKAFADAIKYGNHLMVGGVCPSTSTIAESLQWNIWQSFATTP 160
Db	156	ALSNRQRPFFRPHSATLHNPTRVLFERKWKIATIQQTTEVTSTLDDLEERVK 215



OY 173 RTVPSDNAVNPAILKLKHFMRVRVGTLTOD 203

RESULT 14  
ID US-08-480-751-5 STANDARD: PRT: 1085 AA.

AC xxxxxx

Sequence 5, Application US/08480751

CC Patent No. 5858684

CC GENERAL INFORMATION:

CC APPLICANT: Edward F. Nemeth

CC APPLICANT: Edward M. Brown

CC APPLICANT: Steven C. Hebert

CC APPLICANT: Forrest H. Fuller

CC APPLICANT: James E. Garrett, Jr.

CC TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE

CC NUMBER OF SEQUENCES: 20

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Lyon &amp; Lyon

CC STREET: First Interstate World Center

CC STREET: Suite 4700

CC STREET: 633 West Fifth Street

CC CITY: Los Angeles

CC STATE: California

CC COUNTRY: USA

CC ZIP: 90071

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: FASTSEQ

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/480,751

CC FILING DATE: 7 June, 1995

CC CLASSIFICATION: 435

CC PRIOR APPLICATION DATA:

CC PRIOR APPLICATION DATA: including application

CC PRIOR APPLICATION DATA: described below: 9

CC APPLICATION NUMBER: 08/353,784

CC FILING DATE: 9 December, 1994

CC APPLICATION NUMBER: PCT/US/94/12117

CC FILING DATE: 21 October, 1994

CC APPLICATION NUMBER: U.S. 08/292,827

CC FILING DATE: 23 August, 1994

CC APPLICATION NUMBER: U.S. 08/141,248

CC FILING DATE: 22 October, 1993

CC APPLICATION NUMBER: U.S. 08/009,389

CC FILING DATE: 23 February, 1993

CC APPLICATION NUMBER: U.S. 08/017,127

CC FILING DATE: 12 February, 1993

CC APPLICATION NUMBER: U.S. 07/934,161

CC FILING DATE: 21 August, 1992

CC APPLICATION NUMBER: U.S. 07/834,044

CC FILING DATE: 11 February, 1992

CC APPLICATION NUMBER: U.S. 07/749,451

CC FILING DATE: 23 August, 1991

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Heber, Sheldon O.

CC REGISTRATION NUMBER: 38,179

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (213) 489-1600

CC TELEFAX: (213) 955-0440

CC INFORMATION FOR SEQ. ID NO: 5:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 1085 amino acids

CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
SO SEQUENCE 1085 AA; 121170 MW; 6189757 CN;Query Match 2.8%; Score 192; DB 2; Length 1085;  
Best Local Similarity 27.5%; Pred. No. 9,16e-05;  
Matches 25; Conservative 32; Mismatches 34; Indels 0; Gaps 0;

Db 126 LDEFNCSEHPESTIAVVGATGSGISTAVANLGLFYIPQVSYASSRLSNKPKSFL 185

OY 113 LKAFYDAIKYCPHMLMVEGVCPSVTSIIASLQGMNLYQLSFAATPVLADKKKPYPF 172

Db 186 RTINDHQATAMADIIIEFRNMWGTIAAD 216

OY 173 RTVPSDNAVNPAILKLKHFMRVRVGTLTOD 203

RESULT 15  
ID US-08-484-565-5 STANDARD: PRT: 1085 AA.

AC xxxxxx

Sequence 5, Application US/08484565

CC Patent No. 5763569

CC GENERAL INFORMATION:

CC APPLICANT: Edward M. Brown

CC APPLICANT: Steven C. Hebert

CC APPLICANT: James E. Garrett, Jr.

CC TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE

CC NUMBER OF SEQUENCES: 20

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Lyon &amp; Lyon

CC STREET: First Interstate World Center

CC STREET: Suite 4700

CC STREET: 633 West Fifth Street

CC CITY: Los Angeles

CC STATE: California

CC COUNTRY: USA

CC ZIP: 90071

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: FASTSEQ

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/484,565

CC FILING DATE: 7 June, 1995

CC CLASSIFICATION: 435

CC PRIOR APPLICATION DATA:

CC PRIOR APPLICATION DATA: including application

CC PRIOR APPLICATION DATA: described below: 9

CC APPLICATION NUMBER: 08/353,784

CC FILING DATE: 9 December, 1994

CC APPLICATION NUMBER: PCT/US/94/12117

CC FILING DATE: 21 October, 1994

CC APPLICATION NUMBER: U.S. 08/292,827

CC FILING DATE: 23 August, 1994

CC APPLICATION NUMBER: U.S. 08/141,248

CC FILING DATE: 22 October, 1993

CC APPLICATION NUMBER: U.S. 08/009,389

CC FILING DATE: 23 February, 1993

CC APPLICATION NUMBER: U.S. 08/017,127

CC FILING DATE: 12 February, 1993

CC APPLICATION NUMBER: U.S. 07/934,161

CC FILING DATE: 21 August, 1992

CC APPLICATION NUMBER: U.S. 07/834,044

CC FILING DATE: 11 February, 1992



	PRIOR APPLICATION DATA:	described below:	9
CC	APPLICATION NUMBER:	08/353,784	
CC	FILING DATE:	9 December, 1994	
CC	APPLICATION NUMBER:	PCT/US/94/12117	
CC	FILING DATE:	21 October, 1994	
CC	APPLICATION NUMBER:	U.S. 08/292,827	
CC	FILING DATE:	23 August, 1994	
CC	APPLICATION NUMBER:	U.S. 08/141,248	
CC	FILING DATE:	22 October, 1993	
CC	APPLICATION NUMBER:	U.S. 08/009,389	
CC	FILING DATE:	23 February, 1993	
CC	APPLICATION NUMBER:	U.S. 08/017,127	
CC	FILING DATE:	12 February, 1993	
CC	APPLICATION NUMBER:	U.S. 07/934,161	
CC	FILING DATE:	21 August, 1992	
CC	APPLICATION NUMBER:	U.S. 07/834,044	
CC	FILING DATE:	11 February, 1992	
CC	APPLICATION NUMBER:	U.S. 07/749,451	
CC	FILING DATE:	23 August, 1991	
CC	ATTORNEY/AGENT INFORMATION:		
CC	NAME:	Hebert, Sheldon O.	
CC	REGISTRATION NUMBER:	38,179	
CC	REFERENCE/DOCKET NUMBER:	213/005	
CC	TELECOMMUNICATION INFORMATION:		
CC	TELEPHONE:	(213) 489-1600	
CC	TELEFAX:	(213) 955-0440	
CC	TELEX:	67-3510	
CC	INFORMATION FOR SEQ ID NO:	7:	
CC	SEQUENCE CHARACTERISTICS:		
CC	LENGTH:	1078 amino acids	
CC	TYPE:	amino acid	
CC	TOPOLOGY:	linear	
CC	MOLECULE TYPE:	protein	
SQ	SEQUENCE	1078 AA; 120573 MW; 6153012 CN;	
Dq	Query Match	2.8%; Score 194; DB 1; Length 1078;	
Bd	Best Local Similarity	28.6%; Pred. No. 6,67e-05;	
Md	Matches	26; Conservative 31; Mismatches 34; Indels 0; Gaps 0;	
Db	125 LDFEFCNSEHISTIAVVGATGSGSTAVNVLGLFYIPOVSYASSSRLLSNRNQEKSF	184	
Oy	113 LKARYDAIKYCPNLHWFGGVCSPTSILASLQGWLVLQSFATTPVLADKKRYFF	172	
Db	185 RTPNDEHQATAADIIETFRMMNVGIAD	215	
Oy	173 RVPSDNAVNPAIILKLKHFWRRRVGTLOD	203	
Rt	RESULT 12		
Xx	US-08-480-751-7	STANDARD:	PRT: 1078 AA.
Xx	xxxxxx		
Dt			
Xx	Sequence 7, Application US/08480751		
Dt			
Xx	Patent No. 5858684		
Cc	GENERAL INFORMATION:		
Cc	APPLICANT: Edward F. Nemeth		
Cc	APPLICANT: Edward M. Brown		
Cc	APPLICANT: Steven C. Hebert		
Cc	APPLICANT: Forrest H. Fuller		
Cc	APPLICANT: James E. Garrett, Jr.		
Cc	TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE		
Cc	TITLE OF INVENTION: MOLECULES		
Cc	NUMBER OF SEQUENCES: 20		
Cc	CORRESPONDENCE ADDRESS:		
Cc	ADDRESSEE: Lyon & Lyon		
Cc	STREET: First Interstate World Center		
Cc	STREET: Suite 4700		
Cc	STREET: 633 West Fifth Street		





CC STREET: Suite 4700  
CC STREET: 633 West Fifth Street  
CC CITY: Los Angeles  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 90071  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: FASTSEQ  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/484,565  
CC FILING DATE: 7 June, 1995  
CC CLASSIFICATION: 435  
CC PRIOR APPLICATION DATA:  
CC PRIOR APPLICATION DATA: including application  
CC PRIOR APPLICATION DATA: described below: 9  
CC APPLICATION NUMBER: 08/353,784  
CC FILING DATE: 9 December, 1994  
CC APPLICATION NUMBER: PCT/US/94/12117  
CC FILING DATE: 21 October, 1994  
CC APPLICATION NUMBER: U.S. 08/292,827  
CC FILING DATE: 23 August, 1994  
CC APPLICATION NUMBER: U.S. 08/141,248  
CC FILING DATE: 22 October, 1993  
CC APPLICATION NUMBER: U.S. 08/009,389  
CC FILING DATE: 23 February, 1993  
CC APPLICATION NUMBER: U.S. 08/017,127  
CC FILING DATE: 12 February, 1993  
CC APPLICATION NUMBER: U.S. 07/934,161  
CC FILING DATE: 21 August, 1992  
CC APPLICATION NUMBER: U.S. 07/834,044  
CC FILING DATE: 11 February, 1992  
CC APPLICATION NUMBER: U.S. 07/749,451  
CC FILING DATE: 23 August, 1991  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Heber, Sheldon O.  
CC REGISTRATION NUMBER: 38,179  
CC REFERENCE/DOCKET NUMBER: 213/006  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (213) 489-1600  
CC TELEFAX: (213) 955-0440  
CC TELEX: 67-3510  
CC INFORMATION FOR SEQ ID NO: 8:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 1079 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 1079 AA; 120867 MW; 6054255 CN;  
SQ  
Query Match 2.9%; Score 199; DB 1; Length 1079;  
Best Local Similarity 29.7%; Pred. No. 3.01e-05;  
Matches 27; Conservative 30; Mismatches 34; Indels 0; Gaps 0;  
Db 125 LDEFNCSEHIPSTIAVVGAGSGVSTAVANLGLFIPIQVSYASSSRLLSNKNQYKSF 184  
QY 113 LKAFYDAIKYGNHLMVFGVCPSTVSIASLOGWNLVQLSFAATPVLADKKKYYFF 172  
Db 185 RTIPNDEQATAMADIEYFRNWWGTIAD 215  
QY 173 RTVPSDNAVNPAIILKLFHRWRVGLTOD 203  
RESULT 8  
ID US-08-485-588-8 STANDARD; PRT; 1079 AA.  
XX  
AC xxxxxx  
XX  
DT  
XX  
DE Sequence 8, Application US/08485588

XX  
CC Sequence 8, Application US/08485588  
CC Patent No. 5688938  
CC GENERAL INFORMATION:  
CC APPLICANT: Edward M. Brown  
CC APPLICANT: Steven C. Hebert  
CC APPLICANT: Forrest H. Fuller  
CC APPLICANT: James E. Garrett, Jr.  
CC TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE  
CC NUMBER OF SEQUENCES: 20  
CC CORRESPONDENCE ADDRESSES:  
CC ADDRESSEE: Lyon & Lyon  
CC STREET: First Interstate World Center  
CC STREET: Suite 4700  
CC STREET: 633 West Fifth Street  
CC CITY: Los Angeles  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 90071  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: FASTSEQ  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/485,588  
CC FILING DATE: 7 June, 1995  
CC CLASSIFICATION: 435  
CC PRIOR APPLICATION DATA:  
CC PRIOR APPLICATION DATA: including application  
CC PRIOR APPLICATION DATA: described below: 9  
CC APPLICATION NUMBER: 08/353,784  
CC FILING DATE: 9 December, 1994  
CC APPLICATION NUMBER: PCT/US/94/12117  
CC FILING DATE: 21 October, 1994  
CC APPLICATION NUMBER: U.S. 08/292,827  
CC FILING DATE: 23 August, 1994  
CC APPLICATION NUMBER: U.S. 08/141,248  
CC FILING DATE: 22 October, 1993  
CC APPLICATION NUMBER: U.S. 08/009,389  
CC FILING DATE: 23 February, 1993  
CC APPLICATION NUMBER: U.S. 08/017,127  
CC FILING DATE: 12 February, 1993  
CC APPLICATION NUMBER: U.S. 07/934,161  
CC FILING DATE: 21 August, 1992  
CC APPLICATION NUMBER: U.S. 07/834,044  
CC FILING DATE: 11 February, 1992  
CC APPLICATION NUMBER: U.S. 07/749,451  
CC FILING DATE: 23 August, 1991  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Heber, Sheldon O.  
CC REGISTRATION NUMBER: 38,179  
CC REFERENCE/DOCKET NUMBER: 213/005  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (213) 489-1600  
CC TELEFAX: (213) 955-0440  
CC TELEX: 67-3510  
CC INFORMATION FOR SEQ ID NO: 8:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 1079 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 1079 AA; 120867 MW; 6054255 CN;  
SQ  
Query Match 2.9%; Score 199; DB 1; Length 1079;  
Best Local Similarity 29.7%; Pred. No. 3.01e-05;  
Matches 27; Conservative 30; Mismatches 34; Indels 0; Gaps 0;  
Db 125 LDEFNCSEHIPSTIAVVGAGSGVSTAVANLGLFIPIQVSYASSSRLLSNKNQYKSF 184  
QY 113 LKAFYDAIKYGNHLMVFGVCPSTVSIASLOGWNLVQLSFAATPVLADKKKYYFF 172



CC FILING DATE: 30-DEC-1993  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Parmelee, Steven W.  
 CC REGISTRATION NUMBER: 31,990  
 CC REFERENCE/DOCKET NUMBER: 13952-18-2  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 206-467-9600  
 CC TELEFAX: 415-576-0300  
 CC INFORMATION FOR SEQ ID NO: 2:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 915 amino acids  
 CC TYPE: amino acid  
 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: protein  
 CC SEQUENCE 915 AA; 102231 MW; 4431664 CN;  
 SQ  
 Query Match 3.1%; Score 214; DB 1; Length 915;  
 Best Local Similarity 22.9%; Pred. No. 2,72e-06;  
 Matches 65; Conservative 87; Mismatches 106; Indels 26; Gaps 22;  
 Db 597 LAMGII-ATIFVMAFIRYNDPIYRASGRELSVLLTGIFLCY--IITF-L---MIA- 648  
 Qy 487 LTIIGMMAAFLEFN-IKRNOKLIKMSPPYNNLLIIGMLSYASIFLFGDGSFVSE 545  
 Db 649 KPDVAVCSFRFVFLGLMCISYALLTKTNRIYRIFEOGKSVTAPRLISPTSQLAITSS 708  
 Qy 546 KTFETLCTVFTWILTVGYTAFGAMFAKTWRVHAIFNVKMK-K-KIIDOKLTVYVG 602  
 Db 709 LISVOLGVEI-WGVDPNPIIID-YD-EHKYNNPEQA-RGVYK-CDITDLOI-ICSL-G 761  
 Qy 603 MLTIDL-CILICQWADVPLRRTVERYSMEPDPAGRDISIRPLEHCENHTMTWLGIYVA 661  
 Db 762 YSILIMV-TC-TVYAIKTRGVENENAKPIGFTMTTCIWMLAIFPIFGTAQSAEKLY 819  
 Qy 662 YKGLIMFGCFLEMETRNVSIIPA-LNDSKTYIGMSVYVWGIMCIIGAASVLTROQVVOF 720  
 Db 820 IQTTLTISNLSASVALGMLYMPKRYIIIFHPELVNOKRRSF 863  
 Qy 721 C-IVALVI-I-FCSTIILCLVFEVFKLITLRTNPDATQNRFFOF 761  
 RESULT 4  
 ID US-08-452-734A-2 STANDARD; PRT; 915 AA.  
 AC xxxxxx  
 XX  
 DT  
 XX  
 DE Sequence 2, Application US/08452734A  
 XX  
 CC Sequence 2, Application US/08452734A  
 CC Patent No. 5831047  
 CC GENERAL INFORMATION:  
 CC APPLICANT: Segerson, Thomas P.  
 CC APPLICANT: Kinzie, J. Mark  
 CC APPLICANT: Mulvihill, Eileen R.  
 CC APPLICANT: Saugstad, Julie A.  
 CC APPLICANT: Westbrook, Gary L.  
 CC TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS  
 CC NUMBER OF SEQUENCES: 5  
 CC CORRESPONDENCE ADDRESSES:  
 CC ADDRESSEE: Townsend and Townsend and Crew LLP  
 CC STREET: Two Embarcadero Center, 8th floor  
 CC City: San Francisco  
 CC STATE: CA  
 CC COUNTRY: USA  
 CC ZIP: 94111-3834  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: Patentin Release #1.0, Version #1.25  
 CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/452,734A  
 CC FILING DATE: 30-MAR-1995  
 CC CLASSIFICATION: 435  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 08/176,401  
 CC FILING DATE: 30-DEC-1993  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Parmelee, Steven W.  
 CC REGISTRATION NUMBER: 31,990  
 CC REFERENCE/DOCKET NUMBER: 13952-18-1  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 206-467-9600  
 CC TELEFAX: 415-576-0300  
 CC INFORMATION FOR SEQ ID NO: 2:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 915 amino acids  
 CC TYPE: amino acid  
 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: protein  
 CC SEQUENCE 915 AA; 102231 MW; 4431664 CN;  
 SQ  
 Query Match 3.1%; Score 214; DB 2; Length 915;  
 Best Local Similarity 22.9%; Pred. No. 2,72e-06;  
 Matches 65; Conservative 87; Mismatches 106; Indels 26; Gaps 22;  
 Db 597 LAMGII-ATIFVMAFIRYNDPIYRASGRELSVLLTGIFLCY--IITF-L---MIA- 648  
 Qy 487 LTIIGMMAAFLEFN-IKRNOKLIKMSPPYNNLLIIGMLSYASIFLFGDGSFVSE 545  
 Db 649 KPDVAVCSFRFVFLGLMCISYALLTKTNRIYRIFEOGKSVTAPRLISPTSQLAITSS 708  
 Qy 546 KTFETLCTVFTWILTVGYTAFGAMFAKTWRVHAIFNVKMK-K-KIIDOKLTVYVG 602  
 Db 709 LISVOLGVEI-WGVDPNPIIID-YD-EHKYNNPEQA-RGVYK-CDITDLOI-ICSL-G 761  
 Qy 603 MLTIDL-CILICQWADVPLRRTVERYSMEPDPAGRDISIRPLEHCENHTMTWLGIYVA 661  
 Db 762 YSILIMV-TC-TVYAIKTRGVENENAKPIGFTMTTCIWMLAIFPIFGTAQSAEKLY 819  
 Qy 662 YKGLIMFGCFLEMETRNVSIIPA-LNDSKTYIGMSVYVWGIMCIIGAASVLTROQVVOF 720  
 Db 820 IQTTLTISNLSASVALGMLYMPKRYIIIFHPELVNOKRRSF 863  
 Qy 721 C-IVALVI-I-FCSTIILCLVFEVFKLITLRTNPDATQNRFFOF 761  
 RESULT 5  
 ID PCT-US94-14989-2 STANDARD; PRT; 915 AA.  
 AC xxxxxx  
 XX  
 DT  
 XX  
 DE Sequence 2, Application PC/TUS9414989  
 XX  
 CC Sequence 2, Application PC/TUS9414989  
 CC GENERAL INFORMATION:  
 CC APPLICANT:  
 CC TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS  
 CC NUMBER OF SEQUENCES: 3  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: Patentin Release #1.0, Version #1.25  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: PCT/US94/14989  
 CC FILING DATE:  
 CC CLASSIFICATION:  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 08/176,401  
 CC FILING DATE: 30-DEC-1993  
 CC ATTORNEY/AGENT INFORMATION:



\*\*\*\*\*  
MUSE (TM)  
\*\*\*\*\*

Release 3.1A John F. Collins, Biocomputing Research Unit.  
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Distribution rights by Oxford Molecular Ltd

MPerch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Wed Mar 15 22:31:37 2000; MasPar time 14.90 Seconds  
Tabular output not generated. 817.556 Million cell updates/sec

Title: >US-09-211-755-4  
Description: (1-940) from US09211755.pep  
Perfect Score: 6906  
Sequence: 1 MASPPSSGGPRPPPPPPPPA.....TASPRHRNVPSPFRVWVSGL 940

Scoring table: PAM 150  
Gap 11

Searched: 131253 seqs, 12956647 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-issued  
1:5A\_COMB 2:5B\_COMB 3:PCT9\_COMB 4:backfiles1

Statistics: Mean 37.135; Variance 196.828; scale 0.189

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description	Pred. No.
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1	225	3.3	877	2	US-08-407-		Sequence 2, Applicatio	4.57e-07
2	225	3.3	912	3	PCT-US91-0		Sequence 19, Applicati	4.57e-07
3	214	3.1	915	1	US-08-453-		Sequence 2, Applicatio	2.72e-06
4	214	3.1	915	2	US-08-452-		Sequence 2, Applicatio	2.72e-06
5	214	3.1	915	3	PCT-US94-1		Sequence 2, Applicatio	2.72e-06
6	199	2.9	1079	2	US-08-943-		Sequence 8, Applicatio	3.01e-05
7	199	2.9	1079	1	US-08-484-		Sequence 8, Applicatio	3.01e-05
8	199	2.9	1079	1	US-08-485-		Sequence 8, Applicatio	3.01e-05
9	199	2.9	1079	2	US-08-480-		Sequence 8, Applicatio	3.01e-05
10	194	2.8	1078	1	US-08-484-		Sequence 7, Applicatio	6.67e-05
11	194	2.8	1078	1	US-08-485-		Sequence 7, Applicatio	6.67e-05
12	194	2.8	1078	2	US-08-480-		Sequence 7, Applicatio	6.67e-05
13	194	2.8	1078	2	US-08-483-		Sequence 7, Applicatio	6.67e-05
14	192	2.8	1085	1	US-08-480-		Sequence 5, Applicatio	9.16e-05
15	192	2.8	1085	1	US-08-484-		Sequence 5, Applicatio	9.16e-05
16	192	2.8	1085	1	US-08-485-		Sequence 5, Applicatio	9.16e-05
17	192	2.8	1085	2	US-08-943-		Sequence 5, Applicatio	9.16e-05
18	194	2.8	1088	1	US-08-483-		Sequence 6, Applicatio	6.67e-05
19	194	2.8	1088	2	US-08-480-		Sequence 6, Applicatio	6.67e-05
20	194	2.8	1088	1	US-08-484-		Sequence 6, Applicatio	6.67e-05
21	194	2.8	1088	2	US-08-943-		Sequence 6, Applicatio	6.67e-05
22	194	2.8	1219	2	US-08-687-		Sequence 6, Applicatio	6.67e-05
23	188	2.7	879	1	US-08-486-		Sequence 6, Applicatio	1.72e-04

24	188	2.7	879	1	US-08-072-	Sequence 6, Applicatio	1.72e-04
25	188	2.7	1180	1	US-08-072-	Sequence 8, Applicatio	1.72e-04
26	184	2.7	1180	1	US-08-486-	Sequence 8, Applicatio	3.23e-04
27	188	2.7	1212	1	US-08-072-	Sequence 10, Applicati	1.72e-04
28	184	2.7	1212	1	US-08-486-	Sequence 10, Applicati	3.23e-04
29	181	2.6	877	1	US-08-072-	Sequence 12, Applicati	5.18e-04
30	181	2.6	877	1	US-08-486-	Sequence 12, Applicati	5.18e-04
31	177	2.6	905	1	US-08-072-	Sequence 2, Applicatio	5.18e-04
32	178	2.6	906	1	US-08-486-	Sequence 2, Applicatio	8.27e-04
33	178	2.6	906	3	PCT-US91-0	Sequence 17, Applicati	8.27e-04
34	178	2.6	1056	2	US-08-687-	Sequence 8, Applicatio	8.27e-04
35	178	2.6	1056	2	US-08-687-	Sequence 7, Applicatio	8.27e-04
36	178	2.6	1058	2	US-08-687-	Sequence 5, Applicatio	8.27e-04
37	178	2.6	1199	2	US-08-455-	Sequence 2, Applicatio	8.27e-04
38	178	2.6	1199	2	US-08-465-	Sequence 2, Applicatio	8.27e-04
39	178	2.6	1199	1	US-08-463-	Sequence 2, Applicatio	8.27e-04
40	178	2.6	1199	1	US-08-041-	Sequence 2, Applicatio	8.27e-04
41	178	2.6	1199	3	PCT-US91-0	Sequence 2, Applicatio	8.27e-04
42	118	1.7	533	1	US-08-484-	Sequence 13, Applicati	6.42e+00
43	118	1.7	533	1	US-08-445-	Sequence 10, Applicati	6.42e+00
44	118	1.7	533	1	US-08-484-	Sequence 13, Applicati	6.42e+00
45	118	1.7	533	2	US-08-345-	Sequence 13, Applicati	6.42e+00

## ALIGNMENTS

RESULT 1  
ID US-08-407-875-2 STANDARD: PRT: 877 AA.

AC xxxxxx

Sequence 2, Application US/08407875

Sequence 2, Application US/08407875

Patent No. 5912122

GENERAL INFORMATION:

APPLICANT: Dagget, Lorrie

TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTOR

TITLE OF INVENTION: SUBTYPE mGLuR6, NUCLEIC ACIDS ENCODING SAME AND USES

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

STREET: 444 South Flower Street, Suite 2000

CITY: Los Angeles

STATE: CA

COUNTRY: USA

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/407,875

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Reiter, Stephen E.

REGISTRATION NUMBER: 31,192

REFERENCE/DOCKET NUMBER: P41 9921

TELEPHONE: 619-546-4737

TELEFAX: 619-546-9392

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 877 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein







Best Local	Similarity	28.6%	Pred No.	6,71e-11:	
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				Gaps	0:
Db	125	LDFEFCNCSEHIPSTIAVVGATGCGVSTAAVNLGLFIYPOVYSASSRLSNKNQYSFL	184		
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Qy	113	LKAFYDAIKRGPNHLMVFGVCPYSVSIINAESLOGNNLVLSFAATTPVLADKKKYPYFF	172		
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Qy	173	RTVPSDANVNPALIKLHKFRMRVRGITLTD	203		
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ORGANISM	#formal_name Rattus norvegicus #common_name Norway rat				
DATE	02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 01-May-1998				
ACCESSIONS	159362; A55594				
REFERENCE	159362				
#authors	Ruat, M.; Molliver, M.E.; Snowman, A.M.; Snyder, S.H.				
#journal	Proc. Natl. Acad. Sci. U.S.A. (1995) 92:3161-3165				
#title	Calcium sensing receptor: molecular cloning in rat and localization to nerve terminals.				
#cross-references	MOLDB:95241465				
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REFERENCE	A55594				
#authors	Riccardi, D.; Park, J.; Lee, W.S.; Gamba, G.; Brown, E.M.; Hebert, S.C.				
#journal	Proc. Natl. Acad. Sci. U.S.A. (1995) 92:131-135				
#title	Cloning and functional expression of a rat kidney extracellular calcium/polyvalent cation-sensing receptor.				
#cross-references	MOLDB:95116508				
#accession	A53594				
#molecule_type	mRNA				
#residues	1-133, 'X', 135-1079 ##label RIC				
#cross-references	GB:U10354				
#experimental_source	kidney				
KEYWORDS	calcium; glycoprotein; phosphoprotein; transmembrane protein				
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613-635	#region hydrophobic\				
650-670	#domain transmembrane #status predicted #label TM1\				
683-700	#domain transmembrane #status predicted #label TM2\				
725-744	#domain transmembrane #status predicted #label TM3\				
770-790	#domain transmembrane #status predicted #label TM4\				
806-828	#domain transmembrane #status predicted #label TM5\				
841-860	#domain transmembrane #status predicted #label TM6\				
90,261,287,386,468,	#binding site carbohydrate (Asn) (covalent) #status predicted\				
488,594,893,1005	#binding site phosphate (Ser) (covalent) (by protein kinase C) #status predicted\				
899,901	#binding site phosphate (Ser) (covalent) (by protein kinase A) #status predicted				
SUMMARY	#length 1079 #molecular-weight 120867 #checksum 8153				
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Best Local Similarity	29.7%;	Score 190.3;	47e-11;		
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				Gaps	0;
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	TITLE		#formal_name Arabidopsis thaliana #common_name mouse-ear cress	
	ORGANISM			
	DATE		23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999	
	ACCESSIONS		T05099	
	REFERENCE		ZL5398	
	#authors		Beyan, M.; Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, C. M.; Hohelsel, J.; Wemes, H. W.; Mayer, K.F.X.; Schneller, C.	
	#submission		submitted to the Protein Sequence Database, November 1998	
	#accession		T05099	
	GENETICS		##molecule_type DNA	
	#map_position	4	111/1; 537/1; 634/1; 649/2; 755/3	
	#introns		F28M20.100	
	SUMMARY		#length 898 #molecular_weight 99925 #checksum 6967	
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	Best Local Similarity	30.9%	Pred. No. 6,58e+10;	
	Matches	46; Conservative	36; Mismatches 59; Indels 8; Gaps 7;	
Dd	132	ASFYIEVGOKSQVPIIIFISATSPFL-DGSGPYFRSTYDDSSQVAISEIKIVGVGREV	190	
Qy	138	TSIIAESLOGNMVLQSLFAFTPLADKKRYPFERTPSDNANVPAILKLKLFHRRRV	197	
Dd	191	VPEYEN-NAGEEGIMPGLTDALAINIRIPRKYVISPNATDEISVDLKIMTKPRPVY	249	
Qy	198	GTLTODVORFSE-VRNDLTGLYGEDIEIS-DYE-S-FNSDPCTSVK-KLGNDVRITLL	251	
Dd	250	VHMNFILASRFVESKARETGMLKGAVIIL	278	
Qy	252	GOFDONMAAKAYCCAFESFMGSNTQMII	280	
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	TITLE		parathyroid calcium receptor cDNAs.	
	ORGANISM		19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 17-Mar-1999	
	DATE		A56715	
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	REFERENCE		Garrett, J.E.; Capuano, I.V.; Hammerland, L.G.; Hung, B.C.P.	
	#authors		Brown, E.M.; Hebert, S.C.; Nemeeth, E.F.; Fuller, F.	
	#journal		J. Biol. Chem. (1995) 270(12):919-12925	
	#title		Molecular cloning and functional expression of human parathyroid calcium receptor cDNAs.	
	#cross-references		MUID:95279439	
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KEYWORDS       glycoprotein; neurotransmitter; receptor; transmembrane
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617-637         #domain transmembrane #status predicted #label TM2\
644-664         #domain transmembrane #status predicted #label TM3\
694-714         #domain transmembrane #status predicted #label TM4\
738-759         #domain transmembrane #status predicted #label TM5\
773-794         #domain transmembrane #status predicted #label TM6\
803-827         #domain transmembrane #status predicted #label TM7
SUMMARY        #length 1180 #molecular_weight 129053 #checksum 237


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Best Local Similarity 28.3%; Pred.No.1,66e-13;
Matches            54; Conservative           57; Mismatches    61; Indels   19; Gaps   17


Db              656 AMSYSALVTKTNRIARIAGSK-KKICTKKRPFSACA-OLVIAF-IDIC--IQ-LGITI 708
:::|::||| : | :: ||| : : : : : : : : : |
OY             564 TTAFGAMFAKTVRVAHFENRVMKKKIIXDKDLIVYGMLLIDLCITICQAVDPLRT 623
:::|::||| : | :: ||| : : : : : : : : : |
OY             624 VRYSEMEDPPACRD-I-SIRPLEHCENTHMTIMLGIVAYKGILMIFGC-FIAWETRVVS 681
|-:-|:-| :-| -|:-| : : : : : : : : : |
Db              709 VALFMEPDDIMHDYPSTREYVLIGINTNLGV-VTP-L-GYNGLIL-SCTFYAFTKNVP 765
|-:-|:-| :-| -|:-| : : : : : : : : : |
OY             624 VRYSEMEDPPACRD-I-SIRPLEHCENTHMTIMLGIVAYKGILMIFGC-FIAWETRVVS 681
|-:-|:-| :-| -|:-| : : : : ~~~~~~|
Db              766 -ANFEAKYIAFTVTTCGIMLAEPFI-YFGSNYKLIIIMCF-S-VSL-SATVALGCM-FV 819
:::||::|::| : : : : : : : : : |
OY             682 IPALDSKITIGSYNVNGIMCLTGAAYSFLTRDPDNVOFCIVALAIIFCSITTL-CLAEV 740
:::||::|::| : : : : : : : : : |
Db              820 PKVIIILAPE 830
|--:~::~:~|
OY             741 PRLITLRINPD 751


RESULT          10
ENTRY           JC2131                #type complete
TITLE           metabotropic glutamate receptor 5 B - human
ORGANISM        Homo sapiens #common_name man
DATE            28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change
               05-Jan-1996

ACCESSIONS     JC2131
REFERENCE       JC2131
AUTHORS         Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.
#journal        Biochem. Biophys. Res. Commun. (1994) 199:1136-1143
#title         Molecular cloning and the functional expression of two isoforms of human metabotropic glutamate receptor subtype 5.
#cite          5.

CROSS-REFERENCES MUID:94197696
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##molecule_type mRNA
##residues     1-1212 #label MIN
COMMENT        This protein is coupled to guanine nucleotide binding proteins.
KEYWORDS       glycoprotein; neurotransmitter; receptor; transmembrane
               protein

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617-637         #domain transmembrane #status predicted #label TM2\
644-664         #domain transmembrane #status predicted #label TM3\
694-714         #domain transmembrane #status predicted #label TM4\
738-759         #domain transmembrane #status predicted #label TM5\
773-794         #domain transmembrane #status predicted #label TM6\
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Best Local Similarity 28.3%; Pred.No.1.66e-13;
Matches            54; Conservative           57; Mismatches    61; Indels   19; Gaps   17;
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[illegible]

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Best Local Similarity 56.3%; Pred. No. 0.0054;
Matches 121; Conservative 0; Mismatches 91; Indels 3; Gaps 1

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      11  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      12  GCGCGCCCCGGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC 71
QY      84  GTGCGCTCTGCTGTGGTTGGCGCCGGGGGCGTGGAGCGGGGGGCGCCCGCGCC 143
      11  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      72  GCGCGCACGCGCTTGGCCGCACGACGCGGCCGATATACCGCGCCGGTGGCGCCCG 131
QY      144  GCGCGCCAGCAGCCGCCGCGCTCTCCATCTATGGGCTCTATGCGGCTACACAGAGATGGC 203
      11  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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QY      204  CAAAGGCGAGCATGGGCGGGGGCGTGGTCCCGCGCG 238
      11  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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RESULT 14
US-08-463-092B-3
: Sequence 3, Application US/08463092B
: Patent No. 5768880
: GENERAL INFORMATION:
: APPLICANT: Cole, Susan P.C.
: APPLICANT: Deeleay, Roger G.
:

```

[illegible]



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: March 16, 2000, 09:33:48 ; Search time 6661.37 Seconds

(Without alignments)  
1898.401 Million cell updates/sec

Title: US-09-211-755-3

Perfect score: 2823  
Sequence: 1 ATGGCTTCCCGCCGAGCTC.....TCATGTCTCGGCGCTGTAG 2823

Scoring table: IDENTITY\_NUC

Searched: 4846779 seqs, 2239806763 residues

Database : Pending\_Patents\_NA.\*

Word size : 0

Number of hits that pass the threshold : 9693548

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3	2821.4	99.9	2823	41	US-09-186-664-3			Sequence 3, Appl1	
4	2816.2	99.8	2459	1	PCT-US99-11869-2			Sequence 2, Appl1	
5	2650.4	93.9	2652	1	PCT-US98-22033-3			Sequence 3, Appl1	
6	2650.4	93.9	2652	1	PCT-US98-22033A-3			Sequence 3, Appl1	
7	2650.4	93.9	2652	29	US-08-953-277-3			Sequence 1, Appl1	
8	2348.2	83.2	3480	1	PCT-US99-02361-1			Sequence 1, Appl1	
9	2348.2	83.2	5786	1	PCT-US99-11869-1			Sequence 1, Appl1	
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11	2346.6	83.1	2826	42	US-09-211-755-46			Sequence 46, Appl1	
12	2346.6	83.1	2826	52	US-09-390-134-30			Sequence 30, Appl1	
13	2346.6	82.5	5787	87	US-60-172-373-2106			Sequence 2106, Ap	
14	2311	81.9	3396	1	PCT-US99-11869-28			Sequence 28, Appl1	
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19	2218.2	78.6	3244	29	US-08-953-277-1			Sequence 1, Appl1	
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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21 2218.2 78.6 3244 42 US-09-211-755-1 Sequence 1, Appl1
22 1995.4 70.7 2700 43 PCT-US99-03580-1 Sequence 1, Appl1
23 1995.4 70.7 2887 41 US-09-253-216-1 Sequence 1, Appl1
24 1964.4 69.6 2887 41 US-09-183-253-1 Sequence 1, Appl1
25 1964.4 69.6 2887 91 US-09-502-614-1 Sequence 3, Appl1
26 1061.2 37.6 1318 1 PCT-US99-03580-3 Sequence 3, Appl1
27 1061.2 37.6 1318 41 US-09-183-253-3 Sequence 3, Appl1
28 1061.2 37.6 1318 41 US-09-253-216-3 Sequence 3, Appl1
29 1061.2 37.6 1318 91 US-09-502-614-3 Sequence 3, Appl1
30 743.6 26.3 1171 77 US-60-118-318-209 Sequence 209, App
31 415 14.7 580 47 US-09-307-504-284 Sequence 284, App
32 410.2 14.5 3875 44 US-09-270-767-3 Sequence 3, Appl1
33 410.2 14.5 3968 44 US-09-270-767-12464 Sequence 12464, A
34 410.2 14.5 3666 86 US-60-167-216-346 Sequence 346, App
35 410.2 14.5 3666 86 US-60-168-677-62 Sequence 62, App
36 410.2 14.5 3666 87 US-60-173-383-15286 Sequence 15286, A
37 410.2 14.5 3666 87 US-60-173-464-11965 Sequence 11965, A
38 347.6 12.3 2914 1 PCT-US99-19435-1 Sequence 1, Appl1
39 347.6 12.3 2914 40 US-09-144-779-1 Sequence 1, Appl1
40 347 12.3 2822 1 PCT-US99-09655-1 Sequence 1, Appl1
41 347 12.3 2822 37 US-09-075-463-1 Sequence 1, Appl1
42 347 12.3 3101 41 US-09-194-382-7 Sequence 7, Appl1
43 346 12.3 2886 1 PCT-US99-02361-22 Sequence 22, Appl1
44 346 12.3 2620 19 US-08-756-091-3 Sequence 3, Appl1
45 346 12.3 2620 19 US-08-756-091A-3 Sequence 3, Appl1
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## ALIGNMENTS

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RESULT 1
PCT-US99-19651-3
; Sequence 3, Application PC/TUS9919651
; GENERAL INFORMATION:
; APPLICANT: Symplic Pharmaceutical Corporation
; TITLE OF INVENTION: DNA Encoding a GABBR2 Polypeptide And
; TITLE OF INVENTION: Uses Thereof
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US99/19651
; FILING DATE: Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 54002-E-PCT/JPM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2823 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
PCT-US99-19651-3
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Query Match 100.0%; Score 2823; DB 1; Length 2823;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2823; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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D 1 ATGGCTTCCCGCCGAGCTCCGGGAGCCCGCCGCGCCGCGCCGCGCGCGCG 60
QY 61 CGCGCTGTGTCGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 120
D 1 CGCGCTGTGTCGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 120
QY 61 TGAGAGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTC 180
D 121 TGAGAGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTC 180
QY 181 ATGCGGCTACCAAGAGGTGGCCAAAGGCGAGCATGGGCGGCGGTCTCCCG 240
D 181 ATGCGGCTACCAAGAGGTGGCCAAAGGCGAGCATGGGCGGCGGTCTCCCG 240
QY 241 GAGCTAGCCATGAGAGAGATCCGCAAGGAGTCACTCTGCGCGCGCTGAG 300
D 241 GAGCTAGCCATGAGAGAGATCCGCAAGGAGTCACTCTGCGCGCGCTGAG 300
QY 241 GAGCTAGCCATGAGAGAGATCCGCAAGGAGTCACTCTGCGCGCGCTGAG 300
D 241 GAGCTAGCCATGAGAGAGATCCGCAAGGAGTCACTCTGCGCGCGCTGAG 300
QY 301 CGACTATGACACGAGTGTGACAAATGCAAGGAGTCAAGGAGTCAAGGAGT 360
D 301 CGACTATGACACGAGTGTGACAAATGCAAGGAGTCAAGGAGTCAAGGAGT 360
QY 361 AAGTATGAGCGGCAACCATTTGATGTTGGAGGCGTGTGCGCTGTGACATAT 420
D 361 AAGTATGAGCGGCAACCATTTGATGTTGGAGGCGTGTGCGCTGTGACATAT 420
QY 421 ATGCGGAGTCCCTCCAAAGGCTGATGTGAGAGTCTTCTGCGCGCGCGCT 480
D 421 ATGCGGAGTCCCTCCAAAGGCTGATGTGAGAGTCTTCTGCGCGCGCGCT 480
QY 481 GTTCTTGGGATTAAGAAAGTACCCTGATTTCTCGGAGCGTCCGTCAGACA 540
D 481 GTTCTTGGGATTAAGAAAGTACCCTGATTTCTCGGAGCGTCCGTCAGACA 540
QY 541 GTGACCCCGCCATCTCTGAAGTCTTGAAGCACTTCCGTGGCGGCTGGGCA 600
D 541 GTGACCCCGCCATCTCTGAAGTCTTGAAGCACTTCCGTGGCGGCTGGGCA 600
QY 601 ACCGAGAGCTGAGGCGTCTTCCGAGGTGAGGAATGACCTAGTGGGTTGAT 660
D 601 ACCGAGAGCTGAGGCGTCTTCCGAGGTGAGGAATGACCTAGTGGGTTGAT 660
QY 661 GAAGATATTGATCTCAGACACAGAGAGTTCCTCAATGATCCTGCACAGCT 720
D 661 GAAGATATTGATCTCAGACACAGAGAGTTCCTCAATGATCCTGCACAGCT 720
QY 721 AAGCTCAAGGGGATACGTGGGATCATCTTGGCAATTTGACCAAGATATG 780
D 721 AAGCTCAAGGGGATACGTGGGATCATCTTGGCAATTTGACCAAGATATG 780
QY 781 AAGGTCTTGTGTCGCTTCCGAGGAGAGATGTTGGAGCAAGTATGATATC 840
D 781 AAGGTCTTGTGTCGCTTCCGAGGAGAGATGTTGGAGCAAGTATGATATC 840
QY 841 CCGGATGATGATGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
D 841 CCGGATGATGATGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
QY 901 TGCGTGGAGAGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
D 901 TGCGTGGAGAGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
QY 961 CTGAGCTCCAAATCAATCAAGACCATTCAGGAGAGTCCACACAGATTAAG 1020
D 961 CTGAGCTCCAAATCAATCAAGACCATTCAGGAGAGTCCACACAGATTAAG 1020
QY 1021 TACAACGAGAAAGTTCAAGGCGTGGGCGCCAGCAAGTTCATGAGTACGCT 1080
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Db 1021 TACAAAGCAAAAGCTTGAAGGCTGGGGCCAGCAAGCTTCAAGGCTGAGGCTGAGTGG 1080  
QY 1081 ATCTGGGTCATCGCCAAAGACCTTACAGAGGCCATGAGACACTCATGCCATAGCAGG 1140  
Db 1081 ATCTGGGTCATCGCCAAAGACCTTACAGAGGCCATGAGACACTCATGCCATAGCAGG 1140  
QY 1141 CACGAGGGGATCCAGGACTTCACTACAGAGGCCATGAGACACTCATGCCATAGCAGG 1200  
Db 1141 CACGAGGGGATCCAGGACTTCACTACAGAGGCCATGAGACACTCATGCCATAGCAGG 1200  
QY 1201 GCCATGAGAGAGACCACTTCTCGGGGTCAGGGGTCAAGTTGTCTCCGAGAGGGAG 1260  
Db 1201 GCCATGAGAGAGACCACTTCTCGGGGTCAGGGGTCAAGTTGTCTCCGAGAGGGAG 1260  
QY 1261 AGAATGGAGACCACTTAATTTACTCAATTTCAAGAGAGAGAGAGTGAAGTGGGGGA 1320  
Db 1261 AGAATGGAGACCACTTAATTTACTCAATTTCAAGAGAGAGAGTGAAGTGGGGGA 1320  
QY 1321 TACAAAGCGGCTGACAGACATGAGATCATCATGACACCATGAAGTTCCAGGGTCC 1380  
Db 1321 TACAAAGCGGCTGACAGACATGAGATCATCATGACACCATGAAGTTCCAGGGTCC 1380  
QY 1381 GAGGACCCCAAGAGACAGACATCATCTGGAGACAGCTTGGAGATCTCGCTTCCACTG 1440  
Db 1381 GAGGACCCCAAGAGACAGACATCATCTGGAGACAGCTTGGAGATCTCGCTTCCACTG 1440  
QY 1441 TATAGCATCTGTCCGCTCTACCATCTCGGAGATCATGAGCCAGCCCTTCCCTTC 1500  
Db 1441 TATAGCATCTGTCCGCTCTACCATCTCGGAGATCATGAGCCAGCCCTTCCCTTC 1500  
QY 1501 TTCAACATCAAGAACCGGAAACCAAGCTGATTAAGATGTCAAGCCCTTACATGAAC 1560  
Db 1501 TTCAACATCAAGAACCGGAAACCAAGCTGATTAAGATGTCAAGCCCTTACATGAAC 1560  
QY 1561 CTGATCATCTGGAGAGATGCTGCTGATGATTCATCTTCTTGGCTGAGTGGG 1620  
Db 1561 CTGATCATCTGGAGAGATGCTGCTGATGATTCATCTTCTTGGCTGAGTGGG 1620  
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Db 1621 TCTTCTGCTGAGAAAGACCTTTGAAACACTGTCAGGCTCGGAGCTGATTCAC 1680  
QY 1681 GTGGGCTACACACTGCTTTGGGGCCATTTTGCAAAACCTGAGAGGTCATGCCATC 1740  
Db 1681 GTGGGCTACACACTGCTTTGGGGCCATTTTGCAAAACCTGAGAGGTCATGCCATC 1740  
QY 1741 TTCAAAAATGTGAAGATGAAGAGATCATCAAGACAGACAGCTGTTGTGATG 1800  
Db 1741 TTCAAAAATGTGAAGATGAAGAGATCATCAAGACAGACAGCTGTTGTGATG 1800  
QY 1801 GGGGGCATGCTGCTCATGACCTGTGATCTGTTGGCAGGCTGTGACCCCTG 1860  
Db 1801 GGGGGCATGCTGCTCATGACCTGTGATCTGTTGGCAGGCTGTGACCCCTG 1860  
QY 1861 CGGAGAGACAGTAGAGAGTACAGCATGAGCCGAGCCAGAGCCGGGACATCTCATC 1920  
Db 1861 CGGAGAGACAGTAGAGAGTACAGCATGAGCCGAGCCAGAGCCGGGACATCTCATC 1920  
QY 1921 GGGCCATGCTGAGAACTGGAAGAACCCACATGACATGCTGCTGGCTGCTGAC 1980  
Db 1921 GGGCCATGCTGAGAACTGGAAGAACCCACATGACATGCTGCTGGCTGCTGAC 1980  
QY 1981 GCGTACAAAGGGCTCTCATGCTATGCTGTTGTTCTTGGCATGGGAAACCCGCAATG 2040  
Db 1981 GCGTACAAAGGGCTCTCATGCTATGCTGTTGTTCTTGGCATGGGAAACCCGCAATG 2040  
QY 2041 AGCATCTGCTGCTCAAGAGACAGCATGAGTGGATGAGTGTGACATGTGGGATC 2100  
Db 2041 AGCATCTGCTGCTCAAGAGACAGCATGAGTGGATGAGTGTGACATGTGGGATC 2100  
QY 2101 ATGTGATCATGCGGGCTGCTGCTCTTCTTCAAGCGGTGACAGCCCAAGCTGAGTTC 2160  
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Db 2101 ATGTGATCATGCGGGCTGCTGCTCTTCTTCTGACGCTGACACGCCCAAGCTGCAATT 2160  
QY 2161 TGCATCTGGCCCTGTGATCATCTTTCTGACAGACACATCATCTCTGCTGCTGTTG 2220  
Db 2161 TGCATCTGGCCCTGTGATCATCTTTCTGACAGACACATCATCTCTGCTGCTGTTG 2220  
QY 2221 CCNAGCTCATTTACTGCTGAGGAGCAAAACCTGAGGAGCTGACATGAGAGAGGCTTCAG 2280  
Db 2221 CCNAGCTCATTTACTGCTGAGGAGCAAAACCTGAGGAGCTGACATGAGAGAGGCTTCAG 2280  
QY 2281 TTCAACAGAACCAAGAAAGAGATTTGAAGACTTCCACTTCACTGATGACAGCTGAC 2340  
Db 2281 TTCAACAGAACCAAGAAAGAGATTTGAAGACTTCCACTTCACTGATGACAGCTGAC 2340  
QY 2341 CAGGCGAGACAGTACAGCCCTGGAGGAGCTGAGTGAAGAAACCCGCTTCCGATTAAG 2400  
Db 2341 CAGGCGAGACAGTACAGCCCTGGAGGAGCTGAGTGAAGAAACCCGCTTCCGATTAAG 2400  
QY 2401 ATCAAGAGCTGGACAAAGACTTTGGAAGATGACATGACATGACATGACAGACAGAG 2460  
Db 2401 ATCAAGAGCTGGACAAAGACTTTGGAAGATGACATGACATGACATGACAGACAGAG 2460  
QY 2461 AAGACCATATCATCAAAAGAAATCACTACAAAGAGCTCAAGAGATGCTGAGCTGGG 2520  
Db 2461 AAGACCATATCATCAAAAGAAATCACTACAAAGAGCTCAAGAGATGCTGAGCTGGG 2520  
QY 2521 AACTTCAAGAGAGACAGATGAGAGAAAGGCTATTTTAAATAATCACCTTGATCAAAAC 2580  
Db 2521 AACTTCAAGAGAGACAGATGAGAGAAAGGCTATTTTAAATAATCACCTTGATCAAAAC 2580  
QY 2581 CCCCAGCTCCAGTGAACACAGACAGAGCCCTCAAGACATGCAAGACCCATAGAAAGAC 2640  
Db 2581 CCCCAGCTCCAGTGAACACAGACAGAGCCCTCAAGACATGCAAGACCCATAGAAAGAC 2640  
QY 2641 ATCAACTCCCCGAGACATCCAGCCGCGCTGTGCTGACAGTCTCCATCTTCCACAC 2700  
Db 2641 ATCAACTCCCCGAGACATCCAGCCGCGCTGTGCTGACAGTCTCCATCTTCCACAC 2700  
QY 2701 GCTTACCTCCATCATCGAGGCGGTGATGTCAGCTGTCAGGCTGCTGTCAGCCCT 2760  
Db 2701 GCTTACCTCCATCATCGAGGCGGTGATGTCAGCTGTCAGGCTGCTGTCAGCCCT 2760  
QY 2761 ACCGCGAGCCCTGCGCACAGACAGTACACCTCTTCCGAGTATGATGCTGAGGCTG 2820  
Db 2761 ACCGCGAGCCCTGCGCACAGACAGTACACCTCTTCCGAGTATGATGCTGAGGCTG 2820  
QY 2821 TAG 2823  
Db 2821 TAG 2823

RESULT 2  
US-09-211-755-3  
; Sequence 3, Application US/09211755  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Kenneth A.  
; APPLICANT: Laz, Thomas M.  
; APPLICANT: Borowsky, Beth  
; TITLE OF INVENTION: DNA Encoding a GABABR2 Polypeptide And  
; TITLE OF INVENTION: Uses Thereof  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30





QY 1801 GGGGCGATGCTGCTCAGTACGACCTGTCATCTCTGATCTGTTGGCAGGCTGAGCCCTG 1860  
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DB 1801 GGGGCGATGCTGCTCAGTACGACCTGTCATCTCTGATCTGTTGGCAGGCTGAGCCCTG 1860  
QY 1861 CGGAGGAGAGTGAAGAGGTACGATGAGGCGGAGCCAGCAGGCGGAGCATCTCCATC 1920  
| | | | |  
DB 1861 CGGAGGAGAGTGAAGAGGTACGATGAGGCGGAGCCAGCAGGCGGAGCATCTCCATC 1920  
QY 1921 CGCCCATGCTGGAACACTGCGAAACACCCACATGACATCTGGCTTGGCATTTGTCTAC 1980  
| | | | |  
DB 1921 CGCCCATGCTGGAACACTGCGAAACACCCACATGACATCTGGCTTGGCATTTGTCTAC 1980  
QY 1981 GCCTTCAAGGGGCTCTCTATCTATCTGGGTGTTCTTGGATGGGAACCCCATGTC 2040  
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DB 1981 GCCTTCAAGGGGCTCTCTATCTATCTGGGTGTTCTTGGATGGGAACCCCATGTC 2040  
QY 2041 AGCATCCCTGCCCTCAGACAGCAGTACATCGGCATGAGTGTGTACAAATGTGGGATC 2100  
| | | | |  
DB 2041 AGCATCCCTGCCCTCAGACAGCAGTACATCGGCATGAGTGTGTACAAATGTGGGATC 2100  
QY 2101 ATGTGATCATGCGGGCTGCTGCTCTCTCTCTCTGACGCGTGACCGCCAGCTGCAATC 2160  
| | | | |  
DB 2101 ATGTGATCATGCGGGCTGCTGCTCTCTCTCTCTGACGCGTGACCGCCAGCTGCAATC 2160  
QY 2161 TGCATGCTGGCCCTGCTGATCATCTTCTGACGACATCATCTCTGCTGCTGTTGTG 2220  
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DB 2161 TGCATGCTGGCCCTGCTGATCATCTTCTGACGACATCATCTCTGCTGCTGTTGTG 2220  
QY 2221 CCNAAAGCTATTACTGTGAGCAAAACCCCTGACGCGCAGCTCAGAACAGGCGTTCCAG 2280  
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DB 2221 CCNAAAGCTATTACTGTGAGCAAAACCCCTGACGCGCAGCTCAGAACAGGCGTTCCAG 2280  
QY 2281 TTTCACACAGAACAGAAAGAAAGATTGGAAGACTCTCAGTCTGATGAGGCTGAC 2340  
| | | | |  
DB 2281 TTTCACACAGAACAGAAAGAAAGATTGGAAGACTCTCAGTCTGATGAGGCTGAC 2340  
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| | | | |  
DB 2341 CAGGCGAGCAGCTGACGCTGGAGGAGTGCATGAGAAACACCGCCTTCGATGAG 2400  
QY 2401 ATGACAGAGCTGACAAAGACTTTGGAAGAGTACCATGCTCAGCTCAAGACACCAAG 2460  
| | | | |  
DB 2401 ATGACAGAGCTGACAAAGACTTTGGAAGAGTACCATGCTCAGCTCAAGACACCAAG 2460  
QY 2461 AAGACCAATACATCAAAACGATCTACCAAGAGCTCAAGAGCTCAAGAGCTCAAGAG 2520  
| | | | |  
DB 2461 AAGACCAATACATCAAAACGATCTACCAAGAGCTCAAGAGCTCAAGAGCTCAAGAG 2520  
QY 2521 AACTTCACAGAGCAGACAGATGAGGAAAGGCGCATTTCTAAAAATCAGCTTCATCAAA 2580  
| | | | |  
DB 2521 AACTTCACAGAGCAGACAGATGAGGAAAGGCGCATTTCTAAAAATCAGCTTCATCAAA 2580  
QY 2581 CCCAGCTCAGTGAACACAGACAGCCCTCAAGAAATGCAAAAGCCCATAGAAAG 2640  
| | | | |  
DB 2581 CCCAGCTCAGTGAACACAGACAGCCCTCAAGAAATGCAAAAGCCCATAGAAAG 2640  
QY 2641 ATCAACTCCCCGAGAGCAGATCGAGCCGCGCTGCTCAGCTCCCATCTTCATCAAC 2700  
| | | | |  
DB 2641 ATCAACTCCCCGAGAGCAGATCGAGCCGCGCTGCTCAGCTCCCATCTTCATCAAC 2700  
QY 2701 GCTTACTCCCATCCATCGAGAGGCGTGAATGACAGCTGCTGACGCCCTGTGTGACCCCT 2760  
| | | | |  
DB 2701 GCTTACTCCCATCCATCGAGAGGCGTGAATGACAGCTGCTGACGCCCTGTGTGACCCCT 2760  
QY 2761 ACCGCGAGCCCTCGCCACAGACAGTACACCTCTCTTCCGAGTCAATGGTCTGGGCGCTG 2820  
| | | | |  
DB 2761 ACCGCGAGCCCTCGCCACAGACAGTACACCTCTCTTCCGAGTCAATGGTCTGGGCGCTG 2820  
QY 2821 TAG 2823  
| | |  
DB 2821 TAG 2823

RESULT 3  
US-09-186-664-3  
; Sequence 3, Application US/09186664  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Kenneth A.  
; APPLICANT: Laz, Thomas M.  
; APPLICANT: Borowsky, Beth  
; TITLE OF INVENTION: DNA Encoding a GABAR2 Polypeptide And  
; TITLE OF INVENTION: Uses Thereof  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/186,664  
; FILING DATE: Herewith  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White Esq., John P.  
; REGISTRATION NUMBER: 28,678  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2823 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; US-09-186-664-3  
Query Match 99.9%; Score 2821.4; DB 41; Length 2823;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2822; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ATGGCTTCCCGCGGAGCTCCGCGAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60  
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DB 1 ATGGCTTCCCGCGGAGCTCCGCGAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60  
QY 61 CGCTG 120  
| | | | |  
DB 61 CGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120  
QY 121 TGGAGCGGGGGCG 180  
| | | | |  
DB 121 TGGAGCGGGGGCG 180  
QY 181 ATGCGCTCACAAGAGAGTGGCGCAAGGCGCAGTATCGGGCGGGGCTGCTCCCGCGCTG 240  
| | | | |  
DB 181 ATGCGCTCACAAGAGAGTGGCGCAAGGCGCAGTATCGGGCGGGGCTGCTCCCGCGCTG 240  
QY 241 GAGCTACCATCGAGCAGATCCGCAAGAGTCACTCTGCGCCCTACTTCTCGAGACTG 300  
| | | | |  
DB 241 GAGCTACCATCGAGCAGATCCGCAAGAGTCACTCTGCGCCCTACTTCTCGAGACTG 300  
QY 301 CGACTTATGACACCGAGTGTGACAAATGCAAAAGGAGCTAAAGCCTTTATAGAGCAATA 360  
| | | | |  
DB 301 CGACTTATGACACCGAGTGTGACAAATGCAAAAGGAGCTAAAGCCTTTATAGAGCAATA 360

OY	361	AAAGTATGGGCGAAGCACTTTGATGGTGTGGAGGCGGTGTGCGTCTGTCAACTATT	420
Db	361	AAAGTATGGGCGTGAACCACTTTGATGGTGTGGAGGCGGTGTGCGTCTGTCAACTATT	420
OY	421	ATCGCGGAGTCCCTCCAAAGGCTGGAAATCTGTGACAGCTTTCCTTGCCGCGCACAGCGCT	480
Db	421	ATCCCGGAGTCCCTCCAAAGGCTGGAAATCTGTGACAGCTTTCCTTGCCGCGCACAGCGCT	480
OY	481	GTTCTGTGGGATGAAGAGAGTACCCGTATTTCTTCGGAGCGTCCGTCAGACAAGCG	540
Db	481	GTTCTGTGGGATGAAGAGAGTACCCGTATTTCTTCGGAGCGTCCGTCAGACAAGCG	540
OY	541	GTGAACCCCGCCATCCTGAAGCTCTGAAACACTTCCGCTGGCGCGTGTGGGACACTC	600
Db	541	GTGAACCCCGCCATCCTGAAGCTCTGAAACACTTCCGCTGGCGCGTGTGGGACACTC	600
OY	601	ACGGAGGACGTCAGCGCTCTCCGAGGTGAGAAAGACCTCACTGGGGTTCTGATGG	660
Db	601	ACCGAGGACGTCAGCGCTCTCCGAGGTGAGAAAGACCTCACTGGGGTTCTGATGG	660
OY	661	GAAATATGTAGATCTGACACACAGAGTTTCTCAATGATCCTGCACACAGCGTCAA	720
Db	661	GAAATATGTAGATCTGACACACAGAGTTTCTCAATGATCCTGCACACAGCGTCAA	720
OY	721	AAGCTCAAGGGGAATGACGCGGATCATCCTTGGCGCATTTGACACAAATATGACACA	780
Db	721	AAGCTCAAGGGGAATGACGCGGATCATCCTTGGCGCATTTGACACAAATATGACACA	780
OY	781	AAAGTCTTGTGTGTGCTTCGAGAGAGAGCATGTTTGCGACGAAGTACCACTGGATCATC	840
Db	781	AAAGTCTTGTGTGTGCTTCGAGAGAGAGCATGTTTGCGACGAAGTACCACTGGATCATC	840
OY	841	CCGGAGTGTACGAGCCTGCGTGTGGAGAGAGTGCATGTGGAGGCCAATTCGACAGC	900
Db	841	CCGGAGTGTACGAGCCTGCGTGTGGAGAGAGTGCATGTGGAGGCCAATTCGACAGC	900
OY	901	TGCTGTGGCGAAGACCTCTCTGGCTGCCATGTGGAAGTTAATGAGAGTGGACTTTGAGCC	960
Db	901	TGCTGTGGCGAAGACCTCTCTGGCTGCCATGTGGAAGTTAATGAGAGTGGACTTTGAGCC	960
OY	961	CTGAGCTCCAAACAAATCAAGACCATCTCAGGAGAACTCCACACAGTATGAAAGAG	1020
Db	961	CTGAGCTCCAAACAAATCAAGACCATCTCAGGAGAACTCCACACAGTATGAAAGAG	1020
OY	1021	TTCAAACAGCAACGTTTAGCGCTGTGGGGCCAGCAATTCATGTGGTAAGCCTTAGATGG	1080
Db	1021	TTCAAACAGCAACGTTTAGCGCTGTGGGGCCAGCAATTCATGTGGTAAGCCTTAGATGG	1080
OY	1081	ATCTGGGTCACTGCGCAAGACCTCACAAGAGGGCCATGAAACACTCATCTCAGTAGCAG	1140
Db	1081	ATCTGGGTCACTGCGCAAGACCTCACAAGAGGGCCATGAAACACTCATCTCAGTAGCAG	1140
OY	1141	CACCAAGGATCCAGGACTCACTCACTACAGACACCAAGCCTGGGCAAAATCATCTCAAT	1200
Db	1141	CACCAAGGATCCAGGACTCACTCACTACAGACACCAAGCCTGGGCAAAATCATCTCAAT	1200
OY	1201	GCCATGACGAGACCAACTTCTTCGAGGCTCACGGCTCAAGTGTGTCTCGGAAACGGGAG	1260
Db	1201	GCCATGACGAGACCAACTTCTTCGAGGCTCACGGCTCAAGTGTGTCTCGGAAACGGGAG	1260
OY	1261	AGAATGGGAACCATTAATTTACTCAATTTCAAGACAGAGAGAGTGAAGTGGGCGAA	1320
Db	1261	AGAATGGGAACCATTAATTTACTCAATTTCAAGACAGAGAGAGTGAAGTGGGCGAA	1320
OY	1321	TACAAACGGGTGTGACACACTGAGATCATCAATGACACCATTAAGTTCAGAGGCTCC	1380
Db	1321	TACAAACGGGTGTGACACACTGAGATCATCAATGACACCATTAAGTTCAGAGGCTCC	1380
OY	1381	GAGGACCCCAAGGACAGACCATCTCTGAGAGAGACTTCGGAAAGTCTCGCTTCACTG	1440
Db	1381	GAGGACCCCAAGGACAGACCATCTCTGAGAGAGACTTCGGAAAGTCTCGCTTCACTG	1440

QY	1441	TATGACATCCGTCGCCGTCACATCCGCGAGTATGATGATGCGGACGCCCTCCCTC	1500
QY	1441	TATGACATCCGTCGCCGTCACATCCGCGAGTATGATGATGCGGACGCCCTCCCTC	1500
Db	1441	TATGACATCCGTCGCCGTCACATCCGCGAGTATGATGATGCGGACGCCCTCCCTC	1500
QY	1501	TTCAACATCAAGAACCGGAACAAAAGCTGATTAGATGTCAAGCCCTACATGAACAC	1560
Db	1501	TTCAACATCAAGAACCGGAACAAAAGCTGATTAGATGTCAAGCCCTACATGAACAC	1560
QY	1561	CTCATCATCCGGGAGGAAGTGCCTCTGCATCCATGATCCATCTCTTTGGGCTCGATGG	1620
Db	1561	CTCATCATCCGGGAGGAAGTGCCTCTGCATCCATGATCCATCTCTTTGGGCTCGATGG	1620
QY	1621	TCCTTGCCTCAGAAAAGACCTTTGAACACTGTGACGSGTCCGAACTCGATTCTCAC	1680
Db	1621	TCCTTGCCTCAGAAAAGACCTTTGAACACTGTGACGSGTCCGAACTCGATTCTCAC	1680
QY	1681	GTGGGCTACAAACATGCGCTTTGGGGCCTGATTGTGCAAAACCTGAGGGTCCATCCATC	1740
Db	1681	GTGGGCTACAAACATGCGCTTTGGGGCCTGATTGTGCAAAACCTGAGGGTCCATCCATC	1740
QY	1741	TTCAAAATGTGAAGATGAAGAAGAAGATCATCAAGACCAAGACTGCTGTGATTGTG	1800
Db	1741	TTCAAAATGTGAAGATGAAGAAGAAGATCATCAAGACCAAGACTGCTGTGATTGTG	1800
QY	1801	GGGGGACATGCTGCATCGACGTGCATCTCGATCTGTTGGCAAGCTGTGGACCCCTG	1860
Db	1801	GGGGGACATGCTGCATCGACGTGCATCTCGATCTGTTGGCAAGCTGTGGACCCCTG	1860
QY	1861	CGAGGACATGATGAGAGGTACACATGAGAGCCGGACCCACAGAGCCGGAGCATCTCCATC	1920
Db	1861	CGAGGACATGATGAGAGGTACACATGAGAGCCGGACCCACAGAGCCGGAGCATCTCCATC	1920
QY	1921	CGCCCATGTGCTGSAACACTCGAAACACCCACATGACCATCTGGCTTGGCATGTCTAC	1980
Db	1921	CGCCCATGTGCTGSAACACTCGAAACACCCACATGACCATCTGGCTTGGCATGTCTAC	1980
QY	1981	GCTCAAGAGGGGCTCCCATGATCTATTCGCTGTTCTTGGCATGGGAACCCGCAATGTG	2040
Db	1981	GCTCAAGAGGGGCTCCCATGATCTATTCGCTGTTCTTGGCATGGGAACCCGCAATGTG	2040
QY	2041	AGCATCCCTGCGCTCAACGACAGCATAGTACATGGCATAGTGTGTACAAATGTGGGATC	2100
Db	2041	AGCATCCCTGCGCTCAACGACAGCATAGTACATGGCATAGTGTGTACAAATGTGGGATC	2100
QY	2101	ATNGCATCATCGGGGGCTGTCTCTCTCTCGTAGCGGTGATCAGACCCAGGTGCAGTTC	2160
Db	2101	ATNGCATCATCGGGGGCTGTCTCTCTCTCGTAGCGGTGATCAGACCCAGGTGCAGTTC	2160
QY	2161	TGCATCGTGCGCTGTGCATCATCTTCTGAGACCATACTCTCTGCTGTGTGTGTG	2220
Db	2161	TGCATCGTGCGCTGTGCATCATCTTCTGAGACCATACTCTCTGCTGTGTGTGTG	2220
QY	2221	CCAAAGCATTTATCTGAGAGCAAAACCTGAGCGGCACTCAACAAAGGGGGTTCCAG	2280
Db	2221	CCAAAGCATTTATCTGAGAGCAAAACCTGAGCGGCACTCAACAAAGGGGGTTCCAG	2280
QY	2281	TTCAACAGAAACAGAGAAGAAGATTGGAAGACTCCACTTCCAGTCAACAGCGTGAAC	2340
Db	2281	TTCAACAGAAACAGAGAAGAAGATTGGAAGACTCCACTTCCAGTCAACAGCGTGAAC	2340
QY	2341	CAGGAGACAGTACAGCTGTGAGAGGAGTGCAGTCAAGAAACACAGCGCTTGGAATGAG	2400
Db	2341	CAGGAGACAGTACAGCTGTGAGAGGAGTGCAGTCAAGAAACACAGCGCTTGGAATGAG	2400
QY	2401	ATCACAGAGCTGGCAAAAGACTTGGAAAGATTCACATGACGCTCAAGACACACAGAG	2460
Db	2401	ATCACAGAGCTGGCAAAAGACTTGGAAAGATTCACATGACGCTCAAGACACACAGAG	2460
QY	2461	AAGACACATTCATCAAAAGATTCATCTACACAAAGAGCTCAAGAGATCTCTAGCTTGGC	2520
Db	2461	AAGACACATTCATCAAAAGATTCATCTACACAAAGAGCTCAAGAGATCTCTAGCTTGGC	2520
QY	2521	AACCTCACAGAGACAGATGAGGAAGGCCATTCTTAAAAATCACTCGATCAAAAC	2580

Db	2521	AACTTCACAGAGACACAGATGGGGAAGGCCATTCTAAAAATCACCCTCATCAAAAC	2560
Qy	2581	CCCCAGCTCAGTGGAAACACAGACAGAGCCCTCAGAGAAATGCAAAAGACCCCATAGAAAC	2640
Db	2581	CCCCAGCTCAGTGGAAACACAGACAGAGCCCTCAAGAAATGCAAAAGACCCCATAGAAAC	2640
Qy	2641	ATCAACTCCCCGGAGCAGCAATCCAGCGCCGGCTGTGCCTCAGCTCCCATCCTTCAACAC	2700
Db	2641	ATCAACTCCCCGGAGCAGCAATCCAGCGCCGGCTGTGCCTCAGCTCCCATCCTTCAACAC	2700
Qy	2701	GCTACCTCCCATCATCATCGGAGGCGTGGATGGCAGCTGGGTAGGCCCTGCTACGCCCT	2760
Db	2701	GCTACCTCCCATCATCATCGGAGGCGTGGATGGCAGCTGGGTAGGCCCTGCTACGCCCT	2760
Qy	2761	ACCGCCAGCCCTCGCCACAGACAGCATACCAACCCCTCTTCCAGATCATGGTCTCGGAGCTG	2820
Db	2761	ACCGCCAGCCCTCGCCACAGACAGCATACCAACCCCTCTTCCAGATCATGGTCTCGGAGCTG	2820
Qy	2821	TAG 2823	
Db	2821	TAG 2823	

RESULT 4  
PCT-TS99-11869-2

```

Sequence 2: Application PC/TUS99/11869
GENERAL INFORMATION:
APPLICANT: United States of America, represented by Sec. HHS
APPLICANT: Clark, Janet
APPLICANT: Bonner, Tom I.
TITLE OF INVENTION: Mammalian gb2 GABAB Receptors
FILE REFERENCE: 65879
CURRENT APPLICATION NUMBER: PC/TUS99/11869
CURRENT FILING DATE: 1999-05-28
EARLIER APPLICATION NUMBER: 60/087,274
EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ. ID NOS.: 30
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 3459
TYPE: DNA
ORGANISM: Rattus norvegicus
PCT-US99-11869-2

```

Query Match	99.8%	Score 2816.2;	DB I;	Length 5459;
Best Local Similarity	99.8%	Pred. No. 0;		
Matches 2818; Conservative	1;	Mismatches	4;	Indels 0; Gaps 0;

[illegible]

QY	361	AAATAAGGCGCCGAACCATTTGATGCTGTTTGAGAGCGCTGTCCGTCTGTACATCATATT	420
Db	511	aaatattgagccgaacacatttatgatgttcttgagagcgctctgcctctgtgcacatctatt	570
QY	421	ATCGGAGATCCCTTCGAAGGCTGGAAATCTGATGAGTTTCCTTCGCCGCCACACAGCCT	480
Db	571	atcgcgagagctccctcccaagctcgaaactctgtgaagcttctcttcgcgcgcacacagcct	630
QY	481	GTTCTTGGCGATTAAGAAAGAAATACCCCTTAATTTCTTCGGACGGGTGCCGTCAGACAACGCG	540
Db	631	gtctctcgagataagaagaagtataccgctatttcttcgcgacgctgtgcctcagaacaacgag	690
QY	541	GTTGAACCCCCGCCATCTCTGAAGACTCTCTTAAGACTTCCGCTGCGGGCGGTGGACACTTC	600
Db	691	gtgaacccccgcacatcttgaactctctcttaagacacttccgcctcgagcggtgttgagcaaacct	750
QY	601	ACGCAGACGTGACAGCGCTTCTCCGAGGTGAGGAATATACCTGACTCGGGCTTGATGGG	660
Db	751	acgcagagcggtgcagcgcttctccgaggtgaagaaatgaacctgtcggggttctgtatctgag	810
QY	661	GAGATATTGATCTCAGACACAGAGAGTTTCTTCATGATCCCTGCACACAGCTCAAA	720
Db	811	gaagatatcttgatctcagacacagagaagttcttccaatgatctctgcacacagcgtcaaa	870
QY	721	AAGCTCAAGGGGAATGACGTGGGATCATCTTGCCGCAATGTATACCAAGAAATAGCAGCA	780
Db	871	aagctcaaggggaatgacgtgggatacttgccttgccgcaatgtatatccaagaaatagcagca	930
QY	781	AAAGTCTTCTTTGTGCTTCGAGAGAGCATGTTTGGCAGCAAGTACCAAGTGTGATCATC	840
Db	931	aaagtcttcttgtgtgcttcttgagagagagatgttcttgacgaagatcacagtgatcatc	990
QY	841	CCGGATATGTTACGAGCCTGCGGTGGTGGGACAGTGCATGTGAGAGCCAAATTCCTACGC	900
Db	991	ccggatatgttacgagcctgtcggttgaggacaagtgcatactgtaggcacattctctacgc	1050
QY	901	TGCCGTGCCAACAACCTCTCGGCTGCCATGGAAGTTCATCGAGTGTGACATTTGAGCCC	960
Db	1051	tgccgtgccaagaagcctctcgtcgctgcatactgaaaggttaacatcgtgagtgaactttgagccc	1110
QY	961	CTGAGCTCTCAAAACAATCAAGACCATCTCAGGGAAGACTCTCACAGCATATGAAAGAG	1020
Db	1111	ctgagcttctcaaaaacaatacaagaccatctcagaggaaagactccaacagactttgaagaagag	1170
QY	1021	TACAACACAAACCTTCAGGGGTGGGGCCAGGAAGTCCATGGTATGAGCCCTACACATGGG	1080
Db	1171	tacaacagcaaaagcttcaagcgctgagggccagagatcccatgagcttaagcttaagcttaagctta	1230
QY	1081	ATCTGGGTTCATCGCCAAGAGCCTACAGAGGGCCATGAGACATCGCATCCAGTAGCAG	1140
Db	1231	atctgggttcatcgcccaagaccctacacagagggccatgagagactgtacgtacagtagcagag	1290
QY	1141	CACGACGCGATCCCGAGACTTCACATACACAGACACACAGCTGGGCAAAATCATCCTCAAT	1200
Db	1291	cacgacgcgatcccgagacttcaactaacaagacacaacgcttggccaataatcatctccaat	1350
QY	1201	GCCATGAAACGAGACCACTTCTTCGGGGTACCGGCTCAAGTTGTGTTCCGGAACGGGAG	1260
Db	1351	gccatgaaacgagacacacttcttcggggtacagcggtccaagtgtgttccggagaaaggagag	1410
QY	1261	AGAAATGGGAACCATTAATAATTTACTCAATTTCAAGACAGCAGAGAGGTGAAGGTGGCGGA	1320
Db	1411	agaatgggaaccattaataattactcaaatccaagacagcagagaaggttgaaggttcgagaa	1470
QY	1321	TACAACGGGGGTGTGACACACTGAGGAGATATCAATAGACACCAATAGGTTTCCAGGGGTCC	1380
Db	1471	tacaacgggggtgtgacacactgagagatcatatgaacaacetaaaggttccaaggggtcc	1530
QY	1381	GAGCCACCCAGAGCAAGACCATCATTTCTTGAGACAGCTTCGGAAGATCTCGTCTCCACTG	1440
Db	1531	gagccaccacagagcaagacatcatctctgaaacaacttcgaaagcttccgtctcacggt	1590

QY	1441	TATGAGNCCGTCGTCGTCACATTCGCGATCATATGATGGACGAGCCCTCCTTC	1500
Db	1591	Tatagcatccgtctccctccacatccctclogpatatgacgagccctccctc	1650
QY	1501	TTCAACATCAAGAACCGGAACCAAAAGCTATTAAATGTCAAGCCCTACATGAACAC	1560
Db	1651	ttcaacatcaagaaaccggaacccaagaacgattaaagtatcaagccctacatgaacaac	1710
QY	1561	CTCATCATCCGTGGGAGGAATGCTGCTATGATCCATCTTCTGCTTTGGCCTCGATGG	1620
Db	1711	ctcatcatccgtggaagaatgctgctatgatacatcatctcctcttggcctcgagcgg	1770
QY	1621	TCCCTCGCTCAGAAAGACCTTTGAAACACTGTGACGCGTCCGAGCTGGATTCTCAC	1680
Db	1771	tcctctgctcagaagaagaccttttgaacaacttgcacggtcccgagactgattctcac	1830
QY	1681	GTCGGCTACACAACTGGCTTTGGGGCCATGTTGCAAAACCTGGAGGGTCCATCCCATC	1740
Db	1831	gtgggctacacaactggccttggggccatgtttgcaaaacctggaggggtccatcccatc	1890
QY	1741	TTCAAAATGTAGAGATGAAGAAGAAAGATCATCAAGACAGAACTGCTGTGATTGTG	1800
Db	1891	ttcaaaatgtgaagatgaaagaagaagatcatcaagaaagactgctgtgattgtg	1950
QY	1801	GGGGCATGCTGCTCATACGACTGTGCTATCTGTTGGAGAGCTGTGACCCCTG	1860
Db	1951	ggggcatgctgctcatacgactgtgctatctgttggagagctgtgacccctg	2010
QY	1861	CGGAGGACAGTAGAGAGTACAGATGAGACCGGACCCGACGAGCGCGGGACATCTCCATC	1920
Db	2011	cggaggaacagtggagaggtacacgacgagacggagccgagccggaggaatctccatc	2070
QY	1921	CGCCATTTGCTGGAACACTCGCAAAACACCCACATGACCATCTGGCTTGGCATTTGTCAC	1980
Db	2071	cgcctattgctggaacactcgcaaaaacccacatgacatctgcttggcatttgtctac	2130
QY	1981	GCTTACAGAGGGCTCTCTCATGCTATTTCGGTTGTTTGGCATGGGAACCCGCAATGTG	2040
Db	2131	gcttacaagggctcctccatgctatttcggttcttcttgcatgggaaccgccaatgtg	2190
QY	2041	AGCATCCCTGCCCTCAGACGACGAAAGTACATGGCATGAGTGTACATGTGGGGATC	2100
Db	2191	agcatccctgccctcagacgacgaagtaacatcggaatgtagtgtacatgtggggatc	2250
QY	2101	ATGTGCATCATCGGGCTGCTGCTCTCTCTTCAGCCGTGAGCAGCCCAAGCTGCAGTTC	2160
Db	2251	atgtgcatacatcggggtctgtctctctcttcgaacgctgacagcccaagctgagctc	2310
QY	2161	TGCATCGTGCCCTGTCATCATCTTCTGACGACCATCATCTCTGCTGGTGTGTTGTG	2220
Db	2311	tgcctgctggcctgtcatcatctcttgcagaccatcatctctgtccgtgtgtg	2370
QY	2221	CCAAGGCTATTACTCTGAGGACAAACCCGACGAGCCACATCAGAAAGCGGGTTCCAG	2280
Db	2371	ccaaggctcatctctgaggaacaacccgacgacacatcagaacgaggttccag	2430
QY	2281	TTTCACACGAAACGAGAAGAAAGATTGCAACACCTCCTCACTTCACTGACACGCTGTGAC	2340
Db	2431	ttcacacaggaacgaagaagaagattcgaaagacctccacttcgtatcaacagcgtgtac	2490
QY	2341	CAGGCGACAGCTGACGCTGTGAGGGACTGCACTAGAAAACCAACCGCTTGAAATGAG	2400
Db	2491	caggcgagcagctgacgcgtgagggactgctgaaagaaacacacgcgcttcgaattgag	2550
QY	2401	ATCCACAGGCTGGCAAAAGCTTGGGAAGTACACATCCATCCACTACAGACACACACAG	2460
Db	2551	atccacaggctggcaaaagcttgggaagatcacatgcaagctacaagaacacacagaag	2610
QY	2461	AAGACACATTCATCAAAAGAAATACATTACCAAGAGCTCAAGACATCTCTGCTTGGGC	2520
Db	2611	aagacacatctcatcaaaacgaatcactaccaaagactcaagaaatcctcagcttgggc	2670
QY	2521	AACTTCAAGAGACACAGATGGAAGAAAGCCATTCTAAAAATATCACTCGATCAAAAC	2580

Accession	Sequence	Length
D6	2671 aactccacagagagcacaaagtgtggaagaagccattcttaaaatccacctgcgtcaaaac	2730
QY	2581 CCCAGCCTCCAGTGGAAACAGACAGAGCCCTCAGAACATGCGAAAGACCCATAGAAAC	2640
D6	2731 cccagctccagtgagaaacagacagagccctcaagaacatctgaaagaccocatagaagac	2790
QY	2641 ATCAACTCCCCGGAGACATCCAGCGCCGGCTGTGCTCTCAAGCTCCCATCTTTACAC	2700
D6	2791 atcaactcccgcgagacataccagcgcgcgctgtctcaagctcccatccttcaacac	2850
QY	2701 GCTACACCCCATCATCATCGAGGCGTGGATGCGAGTGGTGCAGGCCCGTGATCGACCT	2760
D6	2851 gctcaactcccatcctcatcgtgaagcgtggaatgcagctgtgttaagcccttgcataagccct	2910
QY	2761 ACCGCACGCCCTCGCCACAGACACAGTACCACCTCTTCCAGTCATGATGTCGGGCTG	2820
D6	2911 acgcgcagccctcgccacagacacagtaacacacctctcttcgagatcatgtctcgggctg	2970
QY	2821 TAG 2823	
D6	2971 tag 2973	

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1      RESULT      5
2      PCT-US98-22033-3
3      Sequence 3, Application PC/TUS9822033
4      GENERAL INFORMATION:
5      APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
6      TITLE OF INVENTION: DNA ENCODING A GABAR2 POLYPEPTIDE AND USES
7      TITLE OF INVENTION: THEREOF
8      NUMBER OF SEQUENCES: 37
9      CORRESPONDENCE ADDRESS:
10     ADDRESSEE: Cooper & Dunham LLP
11     STREET: 1185 Avenue of the Americas
12     CITY: New York
13     STATE: New York
14     COUNTRY: U.S.A.
15     ZIP: 10036
16     COMPUTER READABLE FORM:
17     MEDIUM TYPE: Floppy disk
18     COMPUTER: IBM PC compatible
19     OPERATING SYSTEM: PC-DOS/MS-DOS
20     SOFTWARE: PatentIn Release #1.0, Version #1.30
21     CURRENT APPLICATION DATA:
22     APPLICATION NUMBER: PCT/US98/22033
23     FILING DATE: 16-OCT-1998
24     CLASSIFICATION:
25     ATTORNEY/AGENT INFORMATION:
26     NAME: White, John P.
27     REGISTRATION NUMBER: 28,678
28     REFERENCE/DOCKET NUMBER: 1795/54002-B-PCT/JFM/ADM
29     TELECOMMUNICATION INFORMATION:
30     TELEPHONE: (212) 278-0400
31     TELEFAX: (212) 391-0525
32     INFORMATION FOR SEQ ID NO: 3:
33     SEQUENCE CHARACTERISTICS:
34     LENGTH: 2652 base pairs
35     TYPE: nucleic acid
36     STRANDEDNESS: single
37     TOPOLOGY: linear
38     MOLECULE TYPE: DNA (genomic)
39     HYPOTHEetical: NO
40     ANTI-SENSE: NO
41     PCT-US98-22033-3

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Query Match	93.9%;	Score 2650.4;	DB 1;	Length 2652;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2651; Conservative			Mismatches 1;	Indels 0; Gaps 0;

QY 172 ATGGGCTCATGCCGCTACACAGAGGTGGCCACAGGGCAGACATCGGCGCGCGTACTC 231  
 |||

Db 1 ATGGGCTCATGCCGCTCACCAAGAGGTGGCCAAAGGCGCATCGGGCGGCGTGC 60  
Qy 232 CCCGCCGTTGGAGTCAGGCATGAGACAGATCCGACAGAGCATCTCGGCCCTACTTC 291  
Db 61 CCCGCCGTTGGAGTCAGGCATGAGACAGATCCGACAGAGCATCTCGGCCCTACTTC 120  
Qy 292 CTGACACTGCGACTCTATGACACCGAGTGTGACATGCAAGAGGACTGAAAGCTCTAT 351  
Db 121 CTGACACTGCGACTCTATGACACCGAGTGTGACATGCAAGAGGACTGAAAGCTCTAT 180  
Qy 352 GACGCAATTAAGTATGGGCGCAACCATTTGATGTTGGAGGCGCTGTCCGCTGTC 411  
Db 181 GACGCAATTAAGTATGGGCGCAACCATTTGATGTTGGAGGCGCTGTCCGCTGTC 240  
Qy 412 ACATCTATTATCGGAGATCCCTCCAGGCTGGAATCTGGTGGAGCTTCTCTCGCCGC 471  
Db 241 ACATCTATTATCGGAGATCCCTCCAGGCTGGAATCTGGTGGAGCTTCTCTCGCCGC 300  
Qy 472 ACCAGCGCTGTTCTGGCGGATTAAGAAAGATACCCGATTTCTTCGGAGCGGCGCTCA 531  
Db 301 ACCAGCGCTGTTCTGGCGGATTAAGAAAGATACCCGATTTCTTCGGAGCGGCGCTCA 360  
Qy 532 GACAAAGCGGCTGAACCCGCCATCCTGAAGCTCCTGAAGCATCTTCGCTGGCGGCTGTG 591  
Db 361 GACAAAGCGGCTGAACCCGCCATCCTGAAGCTCCTGAAGCATCTTCGCTGGCGGCTGTG 420  
Qy 592 GGCACACTCAGCGAGAGAGTGCAGCGCTTCTCCGAGGTGAGAAATGACTGATGGGGTT 651  
Db 421 GGCACACTCAGCGAGAGAGTGCAGCGCTTCTCCGAGGTGAGAAATGACTGATGGGGTT 480  
Qy 652 CTGTATGGGGAAGATATTGAGATCTCAGACACAGAGATTTCTCAATGATCCCTGCAC 711  
Db 481 CTGTATGGGGAAGATATTGAGATCTCAGACACAGAGATTTCTCAATGATCCCTGCAC 540  
Qy 712 ACGGCAAAAAGCTCAAGGGAATGAGTGGGATCATCTTGGCCAGTTTGACCAAGAT 771  
Db 541 ACGGCAAAAAGCTCAAGGGAATGAGTGGGATCATCTTGGCCAGTTTGACCAAGAT 600  
Qy 772 ATGGCAGCAAAAGTCTTGTGTGTGCTTCGAGAGAGCATGTTTGGCAGCAAGTACAG 831  
Db 601 ATGGCAGCAAAAGTCTTGTGTGTGCTTCGAGAGAGCATGTTTGGCAGCAAGTACAG 660  
Qy 832 TGGATCATCCCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 891  
Db 661 TGGATCATCCCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720  
Qy 892 TCCTCAGCGTGCCTCGCAGAGAGCTCTGCTGCTCAATGGAAGTTTACATCGAGTGAAC 951  
Db 721 TCCTCAGCGTGCCTCGCAGAGAGCTCTGCTGCTCAATGGAAGTTTACATCGAGTGAAC 780  
Qy 952 TTTGAGCCGCTGAGTCCCAAAACAATCAAGCATCTCAGGAGAAAGTCCACAGCATAT 1011  
Db 781 TTTGAGCCGCTGAGTCCCAAAACAATCAAGCATCTCAGGAGAAAGTCCACAGCATAT 840  
Qy 1012 GAAAGAGATACAGAGCAAAAGTTCAGGCGTGGGGCCCAAGATTCCATGGGTAGGCC 1071  
Db 841 GAAAGAGATACAGAGCAAAAGTTCAGGCGTGGGGCCCAAGATTCCATGGGTAGGCC 900  
Qy 1072 TTAGATGGGATGTGGGTATGCGCCAAAGCCTTACAGAGGCGCATGGAGATACATGCTG 1131  
Db 901 TTAGATGGGATGTGGGTATGCGCCAAAGCCTTACAGAGGCGCATGGAGATACATGCTG 960  
Qy 1132 AGTAGAGGACACAGCGAGTCCAGGATCTCAACTACAGAGCAACAGCTGGGCAAAATC 1191  
Db 961 AGTAGAGGACACAGCGAGTCCAGGATCTCAACTACAGAGCAACAGCTGGGCAAAATC 1020  
Qy 1192 ATCTCTAAATGCCATGAAGAGACCAATCTTTCGGGGGTCAAGGTGATGCTCCGG 1251  
Db 1021 ATCTCTAAATGCCATGAAGAGACCAATCTTTCGGGGGTCAAGGTGATGCTCCGG 1080  
Qy 1252 AACGGGAGAGATGGAGAACCTTAATTTACTCAATTTCAAGACAGACAGAGAGTGAAG 1311  
Db 1081 AACGGGAGAGATGGAGAACCTTAATTTACTCAATTTCAAGACAGACAGAGAGTGAAG 1140

Qy 1312 GTCCGGGAATACAAAGCGGTGGTGTGACACACTGAGATCATCATGACACCATTAAGTTTC 1371  
Db 1141 GTCCGGGAATACAAAGCGGTGGTGTGACACACTGAGATCATCATGACACCATTAAGTTTC 1200  
Qy 1372 CAGGGGTCCGAGCCACCCAGAGACAGACCATATCTTGAGAGCTTTCGAAAGTTCG 1431  
Db 1201 CAGGGGTCCGAGCCACCCAGAGACAGACCATATCTTGAGAGCTTTCGAAAGTTCG 1260  
Qy 1432 CTTTCACTGTATAGATCTGTCCGCTCTCACATCTCTGGCATATGATGATGAGCGCC 1491  
Db 1261 CTTTCACTGTATAGATCTGTCCGCTCTCACATCTCTGGCATATGATGATGAGCGCC 1320  
Qy 1492 TTCTCTTTCTTCAATCAGAACCGGACCAAAAGCTGATTAAGATGTCAGACCCCTAC 1551  
Db 1321 TTCTCTTTCTTCAATCAGAACCGGACCAAAAGCTGATTAAGATGTCAGACCCCTAC 1380  
Qy 1552 ATGAACACCTCATCATCTCTGGAGAAATGCTGTATGATCATCTCTCTCTTGGC 1611  
Db 1381 ATGAACACCTCATCATCTCTGGAGAAATGCTGTATGATCATCTCTCTCTTGGC 1440  
Qy 1612 CTGATGGGTCTCTCTCTCAGAAAAGACCTTTGAANAACCTTGACAGGTCGGACCTGG 1671  
Db 1441 CTGATGGGTCTCTCTCTCAGAAAAGACCTTTGAANAACCTTGACAGGTCGGACCTGG 1500  
Qy 1672 ATTTCACCGTGGGTACACAACCTGCTTGGGGCCATGTTTGAAGAAGCTGGAAGGTC 1731  
Db 1501 ATTTCACCGTGGGTACACAACCTGCTTGGGGCCATGTTTGAAGAAGCTGGAAGGTC 1560  
Qy 1732 CATGCCATCTTCAAAATGTGAAGATGAAGAAGATCATCAAGAACAAGACTGCTT 1791  
Db 1561 CATGCCATCTTCAAAATGTGAAGATGAAGAAGATCATCAAGAACAAGACTGCTT 1620  
Qy 1792 GTGATTTGGGGGGCATGCTGCTATGATGATGATGATGATGATGATGATGATGATG 1851  
Db 1621 GTGATTTGGGGGGCATGCTGCTATGATGATGATGATGATGATGATGATGATGATG 1680  
Qy 1852 GACCCCTCGGAGACAGTGAAGATGACATGGAAGCCGAGACCCAGAGCGCGGAC 1911  
Db 1681 GACCCCTCGGAGACAGTGAAGATGACATGGAAGCCGAGACCCAGAGCGCGGAC 1740  
Qy 1912 ATCTCCATCGGCCCATTTGCTGGAACTGCGAAAACCCACATGACATCTGGTTGAC 1971  
Db 1741 ATCTCCATCGGCCCATTTGCTGGAACTGCGAAAACCCACATGACATCTGGTTGAC 1800  
Qy 1972 ATTGTACGCTTACAGAGGCGCTCTCATGCTATTCGTTGTTTGGCATGGAAAC 2031  
Db 1801 ATTGTACGCTTACAGAGGCGCTCTCATGCTATTCGTTGTTTGGCATGGAAAC 1860  
Qy 2032 CGCAATGTAGCATCCCTGCGCCTCAAGACAGCAAGTACATCGGATGATGATGAT 2091  
Db 1861 CGCAATGTAGCATCCCTGCGCCTCAAGACAGCAAGTACATCGGATGATGATGAT 1920  
Qy 2092 GTGGGATCATGTGATCATCGGGGCTGCTGCTCTTCTGACGCGTGAACGCCAAC 2151  
Db 1921 GTGGGATCATGTGATCATCGGGGCTGCTGCTCTTCTGACGCGTGAACGCCAAC 1980  
Qy 2152 GTGCAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2211  
Db 1981 GTGCAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2040  
Qy 2212 GTGTTTGTGCCAAAGCTCTATCTGTAGGACAAACCTTGACGCGCATCAAGACAG 2271  
Db 2041 GTGTTTGTGCCAAAGCTCTATCTGTAGGACAAACCTTGACGCGCATCAAGACAG 2100  
Qy 2272 CGGTTCCAGTTCACAGAGAACAGAAAGATTCGAAAGACCTTCATTAAGTACAC 2331  
Db 2101 CGGTTCCAGTTCACAGAGAACAGAAAGATTCGAAAGACCTTCATTAAGTACAC 2160  
Qy 2332 AGCGTGAACAGGCGAGCATGCTACGCTGAGAGGAGTGCAGTCAAGAAACACCGCTT 2391  
Db 2161 AGCGTGAACAGGCGAGCATGCTACGCTGAGAGGAGTGCAGTCAAGAAACACCGCTT 2220

QY 2392 CGAATGAGATCATCAGAGCTGTGAGCAAAAGACTGTGAGAAAGTCCATCCATGGAGCTACAGAC 2451  
|  
Db 2221 CGAATGAGATCATCAGAGCTGTGAGCAAAAGACTGTGAGAAAGTCCATCCATGGAGCTACAGAC 2280  
QY 2452 AACACAGAGAGAGACCATATCATATCAAAAGATCTACCAAGAGCTCAACAGACATCTCTC 2511  
|  
Db 2281 AACACAGAGAGAGACCATATCATATCAAAAGATCTACCAAGAGCTCAACAGACATCTCTC 2340  
QY 2512 AGCTTGGGCACTTACAGAGAGAGACAGATGAGAGAAAGCCATCTTAAATAATCACTC 2571  
|  
Db 2341 AGCTTGGGCACTTACAGAGAGAGACAGATGAGAGAAAGCCATCTTAAATAATCACTC 2400  
QY 2572 GATCAAAACCCAGCTCTCACTGAGACAGACAGAGCCCTCAAGAAATGCAAGACCC 2631  
|  
Db 2401 GATCAAAACCCAGCTCTCACTGAGACAGACAGAGCCCTCAAGAAATGCAAGACCC 2460  
QY 2632 ATAGAAGACATCACTCCCGAGACATCCAGAGCCGCTGCTCCAGTCCCATC 2691  
|  
Db 2461 ATAGAAGACATCACTCCCGAGACATCCAGAGCCGCTGCTCCAGTCCCATC 2520  
QY 2692 CTTCACACAGCTTACCTCCATCCATCGAGAGGCTGAGTCCAGCTGAGCCCTGT 2751  
|  
Db 2521 CTTCACACAGCTTACCTCCATCCATCGAGAGGCTGAGTCCAGCTGAGCCCTGT 2580  
QY 2752 GTGAGCCCTACGCGAGCCCTGCGACAGACAGACATCACTCTCTCCAGTCAATGCTC 2811  
|  
Db 2581 GTGAGCCCTACGCGAGCCCTGCGACAGACAGACATCACTCTCTCCAGTCAATGCTC 2640  
QY 2812 TGGGCGCTGTAG 2823  
|  
Db 2641 TGGGCGCTGTAG 2652

RESULT 6  
PCT-US98-22033A-3  
Sequence 3, Application PC/TUS9822033A  
GENERAL INFORMATION:  
APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION  
TITLE OF INVENTION: DNA ENCODING A GABAR2 POLYPEPTIDE AND USES  
TITLE OF INVENTION: THEREOF  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US98/22033A  
FILING DATE: 16-OCT-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 1795/54002-B-PCT/JPW/ADM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 351-0525  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2652 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO

PCT-US98-22033A-3

Query Match 93.9%; Score 2650.4; DB 1; Length 2652;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2651; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 172 ATGGGCTCATGCGGCTTCACCAAGAGAGTGGCCCAAGGGGACAGATCGGGGCGGCTC 231  
|  
Db 1 ATGGGCTCATGCGGCTTCACCAAGAGAGTGGCCCAAGGGGACAGATCGGGGCGGCTC 60  
QY 232 CCCGCGGTGAGCTAGCCATCGAGAGATCGCAACAGAGTACTCTCGCCCTACTTC 291  
|  
Db 61 CCCGCGGTGAGCTAGCCATCGAGAGATCGCAACAGAGTACTCTCGCCCTACTTC 120  
QY 292 CTGGACCTGGACCTCTATGACACCGAGTGTGACATGCAAGAGGAGCTGAAAGCTTCTAT 351  
|  
Db 121 CTGGACCTGGACCTCTATGACACCGAGTGTGACATGCAAGAGGAGCTGAAAGCTTCTAT 180  
QY 352 GACGCAATAAAGTATGAGGCGCAACATTTGATGTGTGGAAGCGTCTGCTGTGTC 411  
|  
Db 181 GACGCAATAAAGTATGAGGCGCAACATTTGATGTGTGGAAGCGTCTGCTGTGTC 240  
QY 412 ACATCTATATCGGGAGTCCCTCCAAAGCTGGAATCTGTGACAGCTTCTCTGCGCGC 471  
|  
Db 241 ACATCTATATCGGGAGTCCCTCCAAAGCTGGAATCTGTGACAGCTTCTCTGCGCGC 300  
QY 472 ACCAGGCTGTCTTCTGGGATTAAGAAAGTACCCGTATTTCTTCCGAGCGTCCGTCA 531  
|  
Db 301 ACCAGGCTGTCTTCTGGGATTAAGAAAGTACCCGTATTTCTTCCGAGCGTCCGTCA 360  
QY 532 GACAAGCGGTGTAACCCCGCATCTGAAGCTCTGAAGCACTTCCGCTGGCGGCTGTG 591  
|  
Db 361 GACAAGCGGTGTAACCCCGCATCTGAAGCTCTGAAGCACTTCCGCTGGCGGCTGTG 420  
QY 592 GGCACTCTACAGAGAGAGTGTGAGGCGCTTCTCCAGGTGAGAGATGACCTGAGGGTT 631  
|  
Db 421 GGCACTCTACAGAGAGAGTGTGAGGCGCTTCTCCAGGTGAGAGATGACCTGAGGGTT 480  
QY 632 CTGTATGGGGAATATTTGATCTCAGACAGAGAGTTTCTCCAAATGATCCCTGCACC 711  
|  
Db 481 CTGTATGGGGAATATTTGATCTCAGACAGAGAGTTTCTCCAAATGATCCCTGCACC 540  
QY 712 AGCGTCAAAAAGCTCAAGGGGATGAGTGGGATCATCTTGGCGAGTTGGACCAAT 771  
|  
Db 541 AGCGTCAAAAAGCTCAAGGGGATGAGTGGGATCATCTTGGCGAGTTGGACCAAT 600  
QY 772 ATGGCAGCAAAAGTCTTCTGTGCTTCAAGAGACATGTTGGCAGCAATACAG 831  
|  
Db 601 ATGGCAGCAAAAGTCTTCTGTGCTTCAAGAGACATGTTGGCAGCAATACAG 660  
QY 832 TGGATCATCCCGGATGTACAGAGCTGCTGTGAGGAGGAGGATGAGAGGCGCAAT 891  
|  
Db 661 TGGATCATCCCGGATGTACAGAGCTGCTGTGAGGAGGAGGATGAGAGGCGCAAT 720  
QY 892 TCCTCAGCTGCTGCGCAGAAAGCTCTGAGTGTGAGAGGTTTACATGAGTGGAC 951  
|  
Db 721 TCCTCAGCTGCTGCGCAGAAAGCTCTGAGTGTGAGAGGTTTACATGAGTGGAC 780  
QY 952 TTTGAGCCCGTGAAGCTCAAAACAAATCAAGACATCTCAGGGAAGAGCTCCACAGCAAT 1011  
|  
Db 781 TTTGAGCCCGTGAAGCTCAAAACAAATCAAGACATCTCAGGGAAGAGCTCCACAGCAAT 840  
QY 1012 GAAAGAGATCAACAGCAAAAGCTTCAAGGCGTGGGGCCAGCAAGTTCCATGGGTACGCC 1071  
|  
Db 841 GAAAGAGATCAACAGCAAAAGCTTCAAGGCGTGGGGCCAGCAAGTTCCATGGGTACGCC 900  
QY 1072 TACGATGGATCTGGGTCATCGCCAGAGACCTACAGAGGCGCATGAGAGACATGATGCC 1131  
|  
Db 901 TACGATGGATCTGGGTCATCGCCAGAGACCTACAGAGGCGCATGAGAGACATGATGCC 960  
QY 1132 AGTAGACGACACAGCGGATTCAGAGACTTCAACTACAGACACACGCTGGCAAAATC 1191  
|  
Db 960 AGTAGACGACACAGCGGATTCAGAGACTTCAACTACAGACACACGCTGGCAAAATC 920

Db 961 AGAGAGGACACAGGAGTCCAGACTTCACTACAGACACAGCGTGGCAAAATC 1020  
Qy 1192 ATCTCAATGCCATAGAGAGACCACTTCTTGGGGTCAAGGTGTGTCGG 1251  
Db 1021 ATCTCAATGCCATAGAGAGACCACTTCTTGGGGTCAAGGTGTGTCGG 1080  
Qy 1252 AACGGGAGAGATGGGAACATTAAATTTACTCAATTTCAAGACAGAGAGTGAAG 1311  
Db 1081 AACGGGAGAGATGGGAACATTAAATTTACTCAATTTCAAGACAGAGAGTGAAG 1140  
Qy 1312 GTTCGGGAATTAACAGCGGTGGCTGACACTGAGATCATCATATGACACATAAGTTT 1371  
Db 1141 GTTCGGGAATTAACAGCGGTGGCTGACACTGAGATCATCATATGACACATAAGTTT 1200  
Qy 1372 CAGGGGTCCGAGCCACCCAAAGAGACATCTTCCTGAGACAGTCCGGAATCTCG 1431  
Db 1201 CAGGGGTCCGAGCCACCCAAAGAGACATCTTCCTGAGAGAGTCCGGAATCTCG 1260  
Qy 1432 CTTCACATGATAGCATCTGTCCCTCTCACCATCTCCGAGATGATGAGCCAGCGC 1491  
Db 1261 CTTCACATGATAGCATCTGTCCCTCTCACCATCTCCGAGATGATGAGCCAGCGC 1320  
Qy 1492 TTCTCTTCTTCAACATCAAGAACCGAAGCAAAAGCTGATTAAGATGTCAGCCCTAC 1551  
Db 1321 TTCTCTTCTTCAACATCAAGAACCGAAGCAAAAGCTGATTAAGATGTCAGCCCTAC 1380  
Qy 1552 ATGAACAACCTCATCTCTGGGAGGAATGCTGTCTATGATCATCTTCTTGGC 1611  
Db 1381 ATGAACAACCTCATCTCTGGGAGGAATGCTGTCTATGATCATCTTCTTGGC 1440  
Qy 1612 CTGATGAGTCTCTGCTCAGAAAAAGACCTTTGAAACATCTCACAGTCCGAGACTGG 1671  
Db 1441 CTGATGAGTCTCTGCTCAGAAAAAGACCTTTGAAACATCTCACAGTCCGAGACTGG 1500  
Qy 1672 ATCTCAACCGTGGGCTACACACATGCTTTGGGGCATGTTTGAAGAGCTTGAAGGTC 1731  
Db 1501 ATCTCAACCGTGGGCTACACACATGCTTTGGGGCATGTTTGAAGAGCTTGAAGGTC 1560  
Qy 1732 CATGCATCTTCAAAATGTAAGATGAAGAAGATCATCAAGACAGAAAGCTGCTT 1791  
Db 1561 CATGCATCTTCAAAATGTAAGATGAAGAAGATCATCAAGACAGAAAGCTGCTT 1620  
Qy 1792 GTGATTTGGGGGGGCTGCTCATCGACCTGTGATCTGATCTGTGGCAGGCTGTG 1851  
Db 1621 GTGATTTGGGGGGGCTGCTCATCGACCTGTGATCTGATCTGTGGCAGGCTGTG 1680  
Qy 1852 GACCCCTGGGAGAGACATAGAGAGTACAGCATGAGCGGACCCAGAGCGCGGAG 1911  
Db 1681 GACCCCTGGGAGAGACATAGAGAGTACAGCATGAGCGGACCCAGAGCGCGGAG 1740  
Qy 1912 ATCTCCATCCGCCATGCTGTGAACATGCGAAAAACCCACATGACCATGTGGCTTGGC 1971  
Db 1741 ATCTCCATCCGCCATGCTGTGAACATGCGAAAAACCCACATGACCATGTGGCTTGGC 1800  
Qy 1972 ATTGTACGCTACAAAGGGGCTCCATGATCGGTTGTCTTGGCATGGGAACC 2031  
Db 1801 ATTGTACGCTACAAAGGGGCTCCATGATCGGTTGTCTTGGCATGGGAACC 1860  
Qy 2032 CGCAATGTAGCATCCCTGCTCAACGACACAAAGTACATCGGATGAGTGTACAAT 2091  
Db 1861 CGCAATGTAGCATCCCTGCTCAACGACACAAAGTACATCGGATGAGTGTACAAT 1920  
Qy 2092 GTGGGATCATGTGCATCATCGGGGTGCTGTCTCTTCTGACGCGTGAACCCCAAC 2151  
Db 1921 GTGGGATCATGTGCATCATCGGGGTGCTGTCTCTTCTGACGCGTGAACCCCAAC 1980  
Qy 2152 GTGCATTTGTCATCGTGGCCCTGGTCATCATCTTCTGACAGCATCTCTGCTG 2211  
Db 1981 GTGCATTTGTCATCGTGGCCCTGGTCATCATCTTCTGACAGCATCTCTGCTG 2040  
Qy 2212 GTGTTTGTGCAAAAGCTCATCTAGAGAGCAAAAGCTGAGAGCGCCACACAGAG 2271  
Db 2041 GTGTTTGTGCAAAAGCTCATCTAGAGAGCAAAAGCTGAGAGCGCCACACAGAG 2100

Qy 2272 CGGTTCCAGTTCACACAGACAGCAAGAAAGATTCGAAGAGCTTCAGTTCAGC 2331  
Db 2101 CGGTTCCAGTTCACACAGACAGCAAGAAAGATTCGAAGAGCTTCAGTTCAGC 2160  
Qy 2332 AGCTTAACCCAGCGAGCAGCATCTACGCTGAGGAGTGCATGAGAAAACCGCTT 2391  
Db 2161 AGCTTAACCCAGCGAGCAGCATCTACGCTGAGGAGTGCATGAGAAAACCGCTT 2220  
Qy 2392 CGAATGAGATCAGAGAGTGGCAAAAGCTTGGAAAGTCAATGACATGACATGAAG 2451  
Db 2221 CGAATGAGATCAGAGAGTGGCAAAAGCTTGGAAAGTCAATGACATGACATGAAG 2280  
Qy 2452 ACACGAGAGAGACACATATCATCAACGAATCATCAAGAGCTCAAGACATCTC 2511  
Db 2281 ACACGAGAGAGACACATATCATCAACGAATCATCAAGAGCTCAAGACATCTC 2340  
Qy 2512 AGCTTGGGCACTTCACAGAGAGCAGATGAGAGAAAGGCTTCAAAATACCTC 2571  
Db 2341 AGCTTGGGCACTTCACAGAGAGCAGATGAGAGAAAGGCTTCAAAATACCTC 2400  
Qy 2572 GATCAAAACCCCGAGCTCCAGTGAACACAGACAGAGCCCTCAAGACATCCAAAGCC 2631  
Db 2401 GATCAAAACCCCGAGCTCCAGTGAACACAGACAGAGCCCTCAAGACATCCAAAGCC 2460  
Qy 2632 ATGAAGACATCAACTCCCGAGAGACATCCAGCGCGGCTGTGCTCCAGTCCCATC 2691  
Db 2461 ATGAAGACATCAACTCCCGAGAGACATCCAGCGCGGCTGTGCTCCAGTCCCATC 2520  
Qy 2692 CTTCACACGCTCACTCCATCCATCGAGAGCGTGTGATGCTGCTGCTCCAGTCCCATC 2751  
Db 2521 CTTCACACGCTCACTCCATCCATCGAGAGCGTGTGATGCTGCTGCTCCAGTCCCATC 2580  
Qy 2752 GTGAGCCCTACGCGCGAGCCCTGCGCACAGACAGACAGTACACCTCTCCAGTACATGTC 2811  
Db 2581 GTGAGCCCTACGCGCGAGCCCTGCGCACAGACAGTACACCTCTCTCCAGTACATGTC 2640  
Qy 2812 TCGGGCTGTAG 2823  
Db 2641 TCGGGCTGTAG 2652

RESULT 7  
US-08-953-277-3  
; Sequence 3, Application US/08953277  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Kenneth A.  
; TITLE OF INVENTION: DNA ENCODING A GABAR2 POLYPEPTIDE AND USES  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/953,277  
; FILING DATE: 17-OCT-1997  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 1795/54002/JPW/KDB  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525



; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2652 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
US-08-953-277-3

Query Match 93.9%; Score 2650.4; DB 29; Length 2652;  
Best local similarity 100.0%; Pred. No. 0;  
Matches 2651; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 172 ATGGGCTCATGCGCTCCGACCAAGAGGTGGCCAAAGGCGACGATCCGGGCGCGCGCTGCTC 231  
Db 1 ATGGGCTCATGCGCTCCGACCAAGAGGTGGCCAAAGGCGACGATCCGGGCGCGCGCTGCTC 60  
QY 232 CCGCGCTGAGAGTACCATCGAGCAGATCCGCAAGCAGATCCTCTGCGCCCTACTTC 291  
Db 61 CCGCGCTGAGAGTACCATCGAGCAGATCCGCAAGCAGATCCTCTGCGCCCTACTTC 120  
QY 292 CTGACCTCGAGCTCATGACACGAGTGTGACATGCAATGCAAGGAGCTGAAAGCTTCTAT 351  
Db 121 CTGACCTCGAGCTCATGACACGAGTGTGACATGCAATGCAAGGAGCTGAAAGCTTCTAT 180  
QY 352 GAGCAATAAAGTATGGGCGCAACATTTGATGTTTGGAGCGTGTGCTGCTGTC 411  
Db 181 GAGCAATAAAGTATGGGCGCAACATTTGATGTTTGGAGCGTGTGCTGCTGTC 240  
QY 412 ACATCATATATGCGGAGATCCCTCCAAAGCTGGAATCGGAGCTTCTGCTGCGCGC 471  
Db 241 ACATCATATATGCGGAGATCCCTCCAAAGCTGGAATCGGAGCTTCTGCTGCGCGC 300  
QY 472 ACCAGCCTGCTTCTGCGGATGAAGAAGTACCCGATTTCTTCGCGAGCGTCCGTCA 531  
Db 301 ACCAGCCTGCTTCTGCGGATGAAGAAGTACCCGATTTCTTCGCGAGCGTCCGTCA 360  
QY 532 GACAAAGCGGTGAACCCCGCATCTGTAAGCTCTGAAAGCACTCCGCTGGCGGCTGTG 591  
Db 361 GACAAAGCGGTGAACCCCGCATCTGTAAGCTCTGAAAGCACTCCGCTGGCGGCTGTG 420  
QY 592 GGCACACTACGAGAGCTGACGCGCTTCTCCAGGTGAAGATGACCTGACTGGGTT 651  
Db 421 GGCACACTACGAGAGCTGACGCGCTTCTCCAGGTGAAGATGACCTGACTGGGTT 480  
QY 652 CTGTATGGGAGATATTGATCTCAGACACAGAGATTCTCCAAATGATCCTGACAC 711  
Db 481 CTGTATGGGAGATATTGATCTCAGACACAGAGATTCTCCAAATGATCCTGACAC 540  
QY 712 AGGCTCAAAAAGTCAAGGGGAATGACGTGGGATCATCTTGCCAGTTTGACAGAAAT 771  
Db 541 AGGCTCAAAAAGTCAAGGGGAATGACGTGGGATCATCTTGCCAGTTTGACAGAAAT 600  
QY 772 ATGGCAGCAAAAAGTCTTCTGTGTGCTTCGAGAGAGAGATGTTTGCGACAGTACAG 831  
Db 601 ATGGCAGCAAAAAGTCTTCTGTGTGCTTCGAGAGAGAGATGTTTGCGACAGTACAG 660  
QY 832 TGGATATATCCCGGAGATGATGACAGGCTCGTGTGGAGAGAGTGTGAGAGGCAAT 891  
Db 661 TGGATATATCCCGGAGATGATGACAGGCTCGTGTGGAGAGAGTGTGAGAGGCAAT 720  
QY 892 TCCCTACGCTGCTGCGCAGAAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 951  
Db 721 TCCCTACGCTGCTGCGCAGAAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
QY 952 TTTGAGCCCTGAGCTCCCAACAAATCAAGACATCTCAAGGAAAGTCTCCACAGAGTAT 1011  
Db 781 TTTGAGCCCTGAGCTCCCAACAAATCAAGACATCTCAAGGAAAGTCTCCACAGAGTAT 840  
QY 1012 GAAAGAGATACAAAGCAAAAGCTTCAGGCGTGGGGCCCAAGCAATTCATGGGTACGCC 1071

Db 841 GAAAGAGATACAAAGCAAAAGCTTCAGGCGTGGGGCCCAAGCAATTCATGGGTACGCC 900  
QY 1072 TAGATGGGATCTGGTTCATGCGCAAGACCTTACAGAGGAGCCATGAGACCTCATGCC 1131  
Db 901 TAGATGGGATCTGGTTCATGCGCAAGACCTTACAGAGGAGCCATGAGACCTCATGCC 960  
QY 1132 AGTACAGGACACAGCGGATTCAGAGACTTACACTACAGACACACCTTGGCAAAATC 1191  
Db 961 AGTACAGGACACAGCGGATTCAGAGACTTACACTACAGACACACCTTGGCAAAATC 1020  
QY 1192 ATCTCAATGCGCATGAACGAGACCAACTTCTCGGGGTACGGGTCAAGTGTTCGG 1251  
Db 1021 ATCTCAATGCGCATGAACGAGACCAACTTCTCGGGGTACGGGTCAAGTGTTCGG 1080  
QY 1252 AACGGGAGAAATGGGAAACATTAATTTACTCAATTTCAAGACAGAGAGTGAAG 1311  
Db 1081 AACGGGAGAAATGGGAAACATTAATTTACTCAATTTCAAGACAGAGAGTGAAG 1140  
QY 1312 GTGCGCAATACAAAGCGGTGCTGACACACTGAGATCATCATGACACCATTAAGTTTC 1371  
Db 1141 GTGCGCAATACAAAGCGGTGCTGACACACTGAGATCATCATGACACCATTAAGTTTC 1200  
QY 1372 CAGGGGTCCGAGCCACCAAGACCAAGACCATCATCTGAGACACTTGGAGATCTCG 1431  
Db 1201 CAGGGGTCCGAGCCACCAAGACCAAGACCATCATCTGAGACACTTGGAGATCTCG 1260  
QY 1432 CTTCACATGATACATCTGTCCGCTCTCACCATCTCCGATGATGATGAGCGCC 1491  
Db 1261 CTTCACATGATACATCTGTCCGCTCTCACCATCTCCGATGATGATGAGCGCC 1320  
QY 1492 TTCCTCTCTCAACATCAAGAACCGGAACCAAAAGCTGATTAAGATGTCAGAGCCCTAC 1551  
Db 1321 TTCCTCTCTCAACATCAAGAACCGGAACCAAAAGCTGATTAAGATGTCAGAGCCCTAC 1380  
QY 1552 ATGAACAACCTCATCATCTGAGAGAGATGCTGCTATGATCATCTTCTCTTGGC 1611  
Db 1381 ATGAACAACCTCATCATCTGAGAGAGATGCTGCTATGATCATCTTCTCTTGGC 1440  
QY 1612 CTGATGGGCTCTCTGCTCAGAAAAGACCTTGAAGACCTTGACAGGTCGCGAGCCGG 1671  
Db 1441 CTGATGGGCTCTCTGCTCAGAAAAGACCTTGAAGACCTTGACAGGTCGCGAGCCGG 1500  
QY 1672 ATTCTACCGGTGCTACACACTGCTTTGGGCGCATGTTTGCAAAACCTGAGAGGTC 1731  
Db 1501 ATTCTACCGGTGCTACACACTGCTTTGGGCGCATGTTTGCAAAACCTGAGAGGTC 1560  
QY 1732 CATGCCATCTTCAAAAATGTAAGATGAAGAAGATCATCAAAAGACCAAGACTGCTT 1791  
Db 1561 CATGCCATCTTCAAAAATGTAAGATGAAGAAGATCATCAAAAGACCAAGACTGCTT 1620  
QY 1792 GTGATTTGGGGGCGATGCTGCTCATGACCTGTGATCTGATCTGTTGGCAGGCTGTG 1851  
Db 1621 GTGATTTGGGGGCGATGCTGCTCATGACCTGTGATCTGATCTGTTGGCAGGCTGTG 1680  
QY 1852 GACCCCTGCGGAGACAGTAGAGGTACAGATGAGACCGAGCCGAGCGGAGAC 1911  
Db 1681 GACCCCTGCGGAGACAGTAGAGGTACAGATGAGACCGAGCCGAGCGGAGAC 1740  
QY 1912 ATCTCCATCCGCCCATTTGTAAGCACTGGAACACCCCAATACCATCTGCTTGGC 1971  
Db 1741 ATCTCCATCCGCCCATTTGTAAGCACTGGAACACCCCAATACCATCTGCTTGGC 1800  
QY 1972 ATTGTCTAGGCTCAAGAGGGCTCTCATGCTATTCGTTGTTTGGCATGGGAAACC 2031  
Db 1801 ATTGTCTAGGCTCAAGAGGGCTCTCATGCTATTCGTTGTTTGGCATGGGAAACC 1860  
QY 2032 GCGAATGTGACATCCCTGCGCTCAAGACAGAAATATATGAGATGATGATGATGAT 2091  
Db 1861 GCGAATGTGACATCCCTGCGCTCAAGACAGAAATATATGAGATGATGATGATGATGAT 1920  
QY 2092 GTGGGATCATGTGATCATATCGGGGCTGCTGCTTCTCTGACCGCTGACACCCAAC 2151



[illegible]

Query Match	83.28;	Score 2348.2;	DB 1;	Length 3480;
Best Local Similarity	89.7%;	Pred. No. 0;		

[illegible]

QY 1078 GGGATCGGTCATGCGCAAGACCTTACAGAGGCGCATGAGACACTGCGATGCCAGTAGC 1137  
1137 ggcattcgtgctatcgcgaagacactcgtgagggccatctgagactcgtatgcagcagc 1432  
QY 1138 AGGCACACCGGATCCAGAGCTTCACTACACAGACACGCTGGGCAAAATCTCTCTC 1137  
1433 cggcaccacggatccaggaactcacaacacgacacgcctggcagagctcctc 1432  
QY 1198 AATGCCATGAGAGACCAACTCTTTCGGGTCACGGGTCACAGTTGTTCGGAACGGG 1257  
1493 aatgcattgagagacacactctcggggtcacgggtcaagtgtatccggaatg 1532  
QY 1258 GAGAGAATGAGGAACATTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1317  
1553 gagaagaatggagacatttaatttaatttaatttaatttaatttaatttaattta 1612  
QY 1318 GAATACACGCGGCTGACACACTGAGATCATCAATGACACCAATTAAGTTCCAGGGG 1377  
1613 gaataacgctgtgacgacacactgagatcatcaatgacacccaatgagttccaagga 1672  
QY 1378 TCCGAGCCACCAAGAGACACATCTTTCGAGAGCTTTCGAGAGATCTCGCTCCA 1437  
1673 tcggaaccccaagaac 1732  
QY 1438 CTGTATAGCATCTGTCGCTCTACACATCTCGGCTGATGATGCGCCAGCGCTTCTC 1497  
1733 ctgtatagcatctctgctctacacatctcctggagatgagttcagttcttctc 1792  
QY 1498 TTCTTCACATCAGAACCGGACCAAAAGCTGATTAAGTATCAAGCCCTTCATGAAAC 1557  
1793 ttcttcacatcagaaacggagatcagatcagatcagatcagatcagatcagatcagat 1852  
QY 1558 AACCTATATCTCTGGAGGAGATGCTGCTGATGATGATGATGATGATGATGATGATG 1617  
1853 aacctatattctctggagagatgctgctgattgattgattgattgattgattgattgatt 1912  
QY 1618 GGGCTCTGCTCAGAAAGACCTTTGAAACACTGTCGAGGTCGGAAGCTGATGATGTC 1677  
1913 ggcctctgctcagaaagacctttgaaacctgtcgagagagagagagagagagagagag 1972  
QY 1678 ACCGTCGTCACACACTCTCTGGGCGATGTTTTCAGAAAGCTGAGGGGTCATGTC 1737  
1973 accgtctgctcacacactctctgggcatgttttcagaaagctgaggggagagagagagag 2032  
QY 1738 ATCTTCAAAAATGTGAGATGAGAGAGATCATCAAGACAGAAAGCTGCTGTGATG 1797  
2033 attctcaaaaatgtgagatgagagagatcatcaagagacagaaactgtgtgagtc 2092  
QY 1798 GTGGGGGCGATGCTGCTACACTGCTGATCTGATCTGATCTGATCTGATCTGATCTG 1857  
2093 gtgggggcatgctgctacactgctgattctgattctgattctgattctgattctgattctg 2152  
QY 1858 CTGCGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAG 1917  
2153 ctgcgagagagagatgagagagatgagagagatgagagagatgagagagatgagagagat 2212  
QY 1918 ATCCGCCATTCGTGGAACACTGCGAAACCCACATGACATCTGCGTTGCAATGTC 1977  
2213 atccgccattctgtggaacctgcgaaacccacatgacatctgctgtgagtcagtc 2272  
QY 1978 TAGCGCTAACAGGGGCTCTGATGATGATGATGATGATGATGATGATGATGATGAT 2037  
2273 tagcgctaacaggggctctgattgattgattgattgattgattgattgattgattgattgatt 2332  
QY 2038 GTAGACATCCCTGCTCAACAGACAGATGATGATGATGATGATGATGATGATGATGATG 2097  
2333 gttagacatccctgctcaacagacagatgattgattgattgattgattgattgattgattgatt 2392  
QY 2098 ATCATGATCATGCGGGGCTGCTGCTCTGATGATGATGATGATGATGATGATGATGATG 2157  
2393 atcatgatcatgcggggctgctgctctgattgattgattgattgattgattgattgattgatt 2452

QY 2158 TTCTGATCGTGGCCCTGGTTCATCTTTCGACACACATCTCTGCTGATGTT 2217  
2453 ttctgattcgtgcttctgttcatctctctcgcagaccatctcctcgtgtatcc 2512  
QY 2218 GTGCCAAGCTCATTCTCTGAGGAAACCTGACGAGCCTGACGAGCCTGAGAGCGGTT 2277  
2513 gtgcgaagctcattctctgaggaacacacacacacacacacacacacacacacacacacac 2572  
QY 2278 CAGTTTCACAGACGAGAGAGAAAGATTGAAAGACTTCACCTTCAGTACACAGCTG 2337  
2573 cagtttctcagatcag 2632  
QY 2338 AACCGAGGAGACGTCAGCGCTGGAGGAGTCACTGAGAAACACACGCTTCGATG 2397  
2633 aaccgagagacgctcagcgctggag 2692  
QY 2398 AAGATCAGAGCTGGACAAAGCTTGGAGAGATGACATGACAGTCAAGACACACA 2457  
2693 aagatcagagctggacaaagcttggagagatgacatgacagctgacagagacacaca 2752  
QY 2458 GAGAGAAGCAGATACATCAAGATCAATCAAGAGTCAAGAGTCAAGAGTCAAGAGTCA 2517  
2753 gagaagaagcagatcacatcaagatcaatcaagagctcagagagagagagagagagagagagag 2812  
QY 2518 GCGAATCTTCACAGAGACACAGATGAGAGAAAGCTTCAAAATCACTGATGATCA 2577  
2813 ggaacttctcagagagacagatgag 2872  
QY 2578 AACCCCGAGCTCAGAGGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2637  
2873 aatcccgagctcag 2932  
QY 2638 GACATCAACTCCCGGAGAGACATCCAGCGCGGCTGAGCGCGAGCGAGCGAGCTTCAC 2697  
2933 gatataactcctcagagac 2992  
QY 2698 CACGCTTACCTCCATCATCGAGGCGTGTGATGATGATGATGATGATGATGATGATGATG 2757  
2993 cagccttacctccatctcctcag 3052  
QY 2758 CCTACGCGCAGAGCTCGCCACAGACAGATGACAGAGAGAGAGAGAGAGAGAGAGAG 2817  
3053 cctacgcgagagctcgccacagacagatgagagagagagagagagagagagagagagagagagag 3112  
QY 2818 CTGTA 2822  
3113 ctgta 3117

RESULT 9  
PCT-US99-11869-1  
; Sequence 1, Application PC/TUS9911869  
; GENERAL INFORMATION:  
; APPLICANT: United States of America, represented by Sec. HHS  
; APPLICANT: Clark, Janet  
; APPLICANT: Bonner, Tom I.  
; TITLE OF INVENTION: Mammalian g2b GABAB Receptors  
; FILE REFERENCE: 65879  
; CURRENT APPLICATION NUMBER: PCT/US99/11869  
; CURRENT FILING DATE: 1999-05-28  
; EARLIER APPLICATION NUMBER: 60/087, 274  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ. ID NOS.: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ. ID NO. 1  
; LENGTH: 5786  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US99-11869-1

Query Match 83.2%; Score 2348.2; DB 1; Length 5786;  
Best Local Similarity 89.7%; Pred. No. 0;



[illegible]



APPLICANT: Jones, Kenneth A.  
 APPLICANT: Laz, Thomas M.  
 APPLICANT: Borowsky, Beth  
 TITLE OF INVENTION: DNA Encoding a GABAR2 Polypeptide and  
 NUMBER OF SEQUENCES: 47  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Cooper & Dunham LLP  
 STREET: 1185 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/211,755  
 FILING DATE: Herewith  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: White Esq./ John P.  
 REGISTRATION NUMBER: 28,678  
 REFERENCE/DOCKET NUMBER: 54002-D  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-278-0400  
 TELEFAX: 212-391-0525  
 INFORMATION FOR SEQ ID NO: 46:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2826 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHEICAL: NO  
 US-09-211-755-46

Query Match 83.1%; Score 2346.6; DB 42; Length 2826;  
 Best Local Similarity 89.7%; Pred. No. 0;  
 Matches 2533; Conservative 0; Mismatches 289; Indels 3; Gaps 1;

Db 421 ATCATGAGAGTCCCTCCAAAGCTGATCTGTGACGCTTCTTGTGCAACACG 480  
 QY CCTGTCTGTGGATTAAGAAAGTACCCGTTCTTCTCGGAGGCGCGTAGACAC 537  
 Db 481 CCTGTCTGTGGATTAAGAAAGTACCCGTTCTTCTCGGAGGCGCGTAGACAC 540  
 QY 538 GCGGTGAACCCCGCATCTGAAGCTCTGAGACACTCCGCTGGCGCGTGTGGACA 597  
 Db 541 GCGGTGAATCCAGCATCTGAAGCTCTGAGACACTCCGCTGGCGCGTGTGGACA 600  
 QY 538 CTCAGCAGACGTCAGCGCTTCTCCAGGTGAGAGTACCTGACTGGGTCTGTAT 657  
 Db 601 CTGACGCAAGACTTCAAGAGTCTGTAGGTGCGGATGACCTGACTGAGTCTGTAT 660  
 QY 658 GGGGAAGTATTGATCTCAGACACAGAGATTTCTCAATGATCCCTGACACGCTC 717  
 Db 661 GCGGAGCATTGATGATTCAGACACGAGACTTCTCAAGATCCCTGACACGCTC 720  
 QY 718 AAAAAGCTCAAGGGGAATGACGTGCGGATCATCTTGGCCAGTTTGACAGAAATATGCA 777  
 Db 721 AAAAAGCTGAAGGGGAATGATGTGCGGATCATCTTGGCCAGTTTGACAGAAATATGCA 780  
 QY 778 GCAAAAGCTTCTGTGTGCTTCGAGAGACATGTTGGCAGCAGTACAGTACGATGAT 837  
 Db 781 GCAAAAGCTTCTGTGTGCTTCGAGAGACATGATGTGTAATATCAATGATGATC 840  
 QY 838 ATCCCGGATGATGACAGCTGCGTGTGGAGACAGTGTGAGGCCAATTCCTCA 897  
 Db 841 ATTCGCGCTGTGTGACAGCTTCTTGTGTGGAGAGTGTGACAGAGGAACTCATC 900  
 QY 898 GCGTGTGCTGCGCAGACACTTCTGCGTGTGAGAGTGTGACAGAGTGTGAGACTTGTAG 957  
 Db 901 GCGTGTGCTGCGCAGACACTTCTGCGTGTGAGAGTGTGACAGAGTGTGAGACTTGTAG 960  
 QY 958 CCCCTGAGCTCCAAACAATCAAGACCATCTCAGGAAAGACTCAGACAGCTATGAAGA 1017  
 Db 961 CCCCTGAGCTCCAAACAAGACCATCTCAGGAAAGACTCAGACAGCTATGAGAGA 1020  
 QY 1018 GAGTACACAGCAACCTTCAAGGCTGTGGGCGCCAGCAAGTTCCATGAGTACGCTCATGAT 1077  
 Db 1021 GAGTACACACAAAGCGGTGACGCTGTGGGCGCCAGCAAGTTCCATGAGTACGCTCATGAT 1080  
 QY 1078 GGGATCTGGTCAATCCGACAGACCTCAGAGAGGCGCATGAGAGACATGATGACAGTAGC 1137  
 Db 1081 GGCATCTGGTCAATCCGACAGACCTCAGAGAGGCGCATGAGAGACATGATGACAGTAGC 1140  
 QY 1138 AGCACAAGCGGATCCAGACTTCAACTACAGACACACAGCTGTGGCAAAATCATCTTC 1197  
 Db 1141 CGGACACAGCGGATCCAGACTTCAACTACAGACACACAGCTGTGGCAAAATCATCTTC 1200  
 QY 1198 AATGCCATGAAGAGACCACTTCTCGGGGTACAGGGTCAAGTTGTTCGGAACGGG 1257  
 Db 1201 AATGCCATGAAGAGACCACTTCTCGGGGTACAGGGTCAAGTTGTTCGGAACGGG 1260  
 QY 1258 GAGAAATGAGAACCATTAATTACTCAATTTCAAGACAGACAGAGGTGAAGTGTGGC 1317  
 Db 1261 GAGAAATGAGAACCATTAATTACTCAATTTCAAGACAGAGAGGTGAAGTGTGGGGA 1320  
 QY 1318 GAATCAACAGCGGTGCTGACACACTGAGATCATCAATGACACCATTAAGTTTCCAGGG 1377  
 Db 1321 GAGTCAACAGCGGTGCTGACACACTGAGATCATCAATGACACCATTAAGTTTCCAGGA 1380  
 QY 1378 TCCGAGCAACCAAGAGCAAGACATCAATTTGAGAGAGCTTCCGAAGATTCGCTTCCA 1437  
 Db 1381 TCCGAGCAACCAAGAGCAAGACATCAATTTGAGAGAGCTTCCGAAGATTCGCTTCACT 1440  
 QY 1438 CTGTATAGCATCTGTCCGCTCACACATCTCGGACATGATATGAGCCAGGCGCTTCTC 1497  
 Db 1441 CTGTACAGCATCTGTCCGCTCACACATCTCGGACATGATATGAGCCAGGCGCTTCTTC 1500  
 QY 1498 TTCTTCAACATCAAGAACCGGAACCAAGCTGATTAAGATGTAAAGCCCTTACATGAAAC 1557





QY	358	AAAGATGAGGGCCCAACATTATGATGTTTGGAGGCGTGTGCGCTGTGCACATCT	411
Dp	361	ataaatatagggccctcaaccacttgaigtgttggaggggtctgttcacgtccatcc	420
QY	418	ATTATGGCGGATCCCTCCAGGCTGGAAATCTGATGTCAGCTTCTCTTGCCGCACACAG	477
Dp	421	atcatctgcagagtcctcccaaggtctggaatctcvgtgcaacttctcttgcgtgcacaaag	480
QY	478	CTGTCTTCTTGGGATTAAGAGAAGTACCCTGATTTCTTCCGACAGGTGCGTGCAGCAAC	537
Dp	481	ccgtctcttcagccgataaagaaaaataaccctattcttcttcggacggtccatcagaacat	540
QY	538	GGGTTAAACCCCGCATCTCTTAAGCTCCTTAACCACTTCTCCGTGGCGGCGTGTGGCAAC	597
Dp	541	ggcgttgatctccagcatctctgaagtgtctgaagcactaccacgtgaagcgcgttgagcaag	600
QY	598	CTCAGCAGAGAGTCACAGCGCTTCTCCGAGATGAGAAATGACCTACAGGGGTTCTGTAT	657
Dp	601	ctgacgcgaagagcttcagaggtctctctgtgaggtgcgaatgacctgactgtagtctgtat	660
QY	658	GGGGAAGATATTGATGATCTGCACACAGACAGATTTCTCCAGTAACTCTGCACACAGTC	717
Dp	661	ggcgaggaactctggaatcttcagacaaccgagagctctcccaagaacccctgcacaggtctc	720
QY	718	AAAAAGCTCAAGGGGATGATGCTGCGATATCTTGGCCAGTTTGACCAAAATATGCA	777
Dp	721	aaaaagctgaagggaggaatggaatgctgagatcatctcttgcaggttgcacgaataatgga	780
QY	778	GCAAAAGCTCTTGTGTGTGCTCTCGAAGAGAGCATTTTGGCAGCAATATACAGTGGATC	837
Dp	781	gcaaaagtctctgtgtgtgtgcatcagagagaacatgtatgagtagtaaatatctagtgatc	840
QY	838	ATCCCGGATATGGATGACAGCGTCGCTGGTGGGAGACAGTGCATGTCGAAGGCCAATTCCTCA	897
Dp	841	atctccgggcgtgtacgagcctctctgtgtggagcaggtgcacacggaagccaactatcc	900
QY	898	CGCTGCCCTCGCAGAAAGCTCCTGGCTGCCATGGAAGTTTAACTGAGATGAGATTTGAG	957
Dp	901	cgcgtccctccggaagaatctctgtctgcgcagcagtgaggggtctaatcttgggttgatcttcgag	960
QY	958	CCCCCTGAGCTCCAAACAAATACAGACATCTCAAGGAGATCTCCACAGCATATGAAGA	1011
Dp	961	ccccctgagctccaagaagcagataaagaacatctccagaaagaatctccacagcatgataagaa	1020
QY	1018	GAGTACACAGCAAAAGCTTTCAGGGCTGGGGCCAGCAAACTTTCATGAGGGTATACGCTTACGAT	1077
Dp	1021	gagtagacaacaacaaggggtccagggcgttgaggccagcaagttccaaaggttaagcctcagat	1080
QY	1078	GGGATCTGGGTCATCGCCAAAGCCCTTCADAGGGCCATGGAACACTGTCAGTCAGAGAG	1133
Dp	1081	ggatctcgggtctctcgcgaagaacactcagaaagggccaatggaacatctgcatgcagcagacg	1144
QY	1138	AGGATCCAGCGGATTCAGAGACTTCAACTATACAGACACACAGCTGTGGCAAAATCATCTTC	1199
Dp	1141	cggagaccagggagctcagaagacttcaactacacagaccacaagcctggggaagaatcaatctc	1200
QY	1198	AATGCCATGACGAGACCAACCTCTCTGGGCTCACGGGTCAAGTTGTCTTCGGAAACGG	1255
Dp	1201	aatgccatgaacgagaaaccaactctctcgggggtcaacgggtcaagttgttatcttcggaatagg	1266
QY	1258	GAGAGATGGGAACATTAAATTATTCATTTCAATTTTCAAGACAGACAGAGATGTAAGATCGCG	1317
Dp	1261	gagagaaatggggaccattaaatttattccaatcttcagaagcagagggaggttgaaagtgtgga	1320
QY	1318	GAATATCAACGGGTGGCTGCACACACTGAGATATCATATCAAGACACATTAAGTTAGTTCAGGG	1377
Dp	1321	gagtagacaagcgtgtggccgagacaacctggaatataatcaatgaacatcatagtttccaagga	1381
QY	1378	TCCGAGCCACCAAGACAAAGATCATTTCTGAGCAACCTTCCGAAAGATCTCGCTTCCA	1433
Dp	1381	tcgcgaaccacaaaagaaacagacatcatctctcggagcagcttgcggaagaatctccctactc	1444
QY	1438	CTGTATAGATCCTGTCCGCTCTACCACTCCTGGGATANTAGTGGACGACGCTTCTCTC	1497

Db	1441	ctctaaagatctctctctgcctctacacatctcccggtatgatcatcagtcagtgctttctc	15000
Oy	1498	tttttttaaatatagaaacccgaacccaaaagctgattagatgtcaaaccccttcatganc	1557
Db	1501	ctctccaaacaaagaaacccggaataacagagctccaaataaagatgctcgaatacaagaac	1566
Oy	1558	aacctcatcatcttgaggagaaatgctctccattgcatccattcttctttggcctcgat	1617
Db	1561	aacctatcatctcttgaggagatgctctctctatgctctccatattctcttggccttgat	1620
Oy	1618	gggtctcttctgctcagaaaagacctttgaaaacactctgcacagctccgagacttgatttc	1677
Db	1621	ggaatctctgctctcgaagaaagaccttggaaaacatttgacgcctcagacctgattctc	1680
Oy	1678	accgtggggtttacacaaactgcctttggggggccattgtttggaaaagaccttgagacatggc	1733
Db	1681	accgtggtctaaacgacctgttttgggcacattgtttgaaagaccttgagajctcaagc	1740
Oy	1738	attcttcaaaaatgtgaatagatgaaagaagatcatcaaaagccagaaagctgcttgatgt	1797
Db	1741	attcttcaaaaatggtgaatagatgaaagaagatcatcaaaagccagaaagctgcttgatc	1800
Oy	1798	gtgggggggcatctgctctcatgacactgtgcatctctgattctgttggaacgcttgacccc	1857
Db	1801	gtgggggggcatctgctctgattgacactgtgtatcttcttccatctctgacagcttgagccc	1860
Oy	1858	ctggcggagagacagatgaaagaggtatagacatgagacccggacccagaccccgacatcttc	1917
Db	1861	ctggagaaagacagatgaaagatagacatgagacccggacccagacccagagatctcttc	1920
Oy	1918	attcggcccaatttcttggaacactgtggaaaacccacatgacacattctggtggcatgttc	1977
Db	1921	attcggccctctcttgagcacttgaggaaacacccatgacacatcttgcttgcatctgc	1980
Oy	1978	ttagccttacaabgggctctctacatctcatttcggctgttcttggaatgggaaaacccgaat	2037
Db	1981	ttagccttacaabgggctctctccatctcttcttcttcttcttcttcttcttcttcttctt	2040
Oy	2038	gtgagacatccctgcctctcaacgacacagacagatgacatgcatgctgttcaattgtgggg	2097
Db	2041	gtgaagatctcccgcatcaataagaaagatgacatctggatgagatgcttacaacagctgggg	2100
Oy	2098	atcatgtgcatcatcgtggggctgctgtctcccttccttcctgcagccggagcccaattgcmg	2157
Db	2101	atcatgtgcatcatcgtggggctgctgtctcccttccttcctgcagccggagcccaattgcmg	2160
Oy	2158	tttgcatgctggccctctggtatcatcttcttgagacacatcatctctctgctgctgctgtt	2217
Db	2161	ttctgctatgctgctctgctgctatcatctctctgagacacatcaacccctctgctgctatcc	2220
Oy	2218	gttcgcgaaccttatttactctgaagacaaacccctgcagccatcttcacacacagcgcttc	2277
Db	2221	gttcgcgaaccttatttactctgaagacaaacccctgcagccatcttcacacacagcgcttc	2280
Oy	2278	caattgcacacagacacagaaagaagatttggaagacctctccacttcagctacacagctgc	2337
Db	2281	caattgcacacagacacagaaagaagatttcctaaacagctccacactctgctacacagctgc	2340
Oy	2338	aaccagggcagacactgcacgctctggaagagctgcagctgcagctgcagctgcagctgcagc	2397
Db	2341	aaccagggcagacactgcacgctctggaagagctgcagctgcagctgcagctgcagctgcagc	2400
Oy	2398	aagatgcacagactctggacaaagatttggaagaaagctacacatgacacgtctacaaacaca	2455
Db	2401	aagatgcacagactctggatataagactctggaagagctgcagctgcagctgcagctgcagc	2466
Oy	2458	gagaaacacacatcaattcaaaacagatctacatcagaaagctcaacgacatctcacttg	2511
Db	2461	gaaagacacacatcaattcaacagaaacacacatcagaaagctcaatgacatctcacttc	2520
Oy	2518	ggcaacttcacagagacacagatgagagaaagccattttaaaaaaatcactcgtatcaa	2577



[illegible]

Dh	698	gttgaacattgcccacacgagacatcccgcaacgagtcactccctcgcccttactcttcgac	757
Oy	298	cttccgacactctatgacacccgagctgga- caattgcAAAGGGACTGAAAGCCTTGTATGAGC	356
Dh	758	cctgcgcctctatgacacgagagtcgancacagcaaaaggttgaagccttctacagatgc	817
Oy	357	AATTAAGTATGGGCGCAACCAATTGATGCTGTTTGAGGCGCTGTCCGTCTGTCAATC	416
Dh	818	aataaattccgagccgacacacttgaattgtttgagagcgtctgtctcatccgttcaatc	877
Oy	417	TATTATCGGAGAGTCCCTCCCAAGGCGAATGTGTGAGCTTCTCCCTGGCCGACAC	476
Dh	878	calcatatgaggtccctcccaagcgtcgatcttgttgagttcttcttgcgtcaaacac	937
Oy	477	GCCTGTTCTTGCGGATTAAGAAAGTACCCGATTTCTTCGGAGCGTGGCGTCAACAA	536
Dh	938	gcccgtctcaagccgataagaaaaaataccctattcttcttcgacgcgtcccaacgaaca	997
Oy	537	CGCGGTGAACCCCGCATCTGAAAGCTCTGTGAAGCACTTCCGCTGGCGGCTGTGGGAC	596
Dh	998	tgcgctgtaatccagccatctctgtaagtgttctcaagaactacacagtgaaagcgttggagac	1057
Oy	597	ACTACGACGAGCGTGCAGCGCTTCTCCAGGTGAGGAAATCACTGTACTGGGTTCTGTA	656
Dh	1058	gctcagcagaacgcttcagaggtcttccttgaggttgcgagatgacctcgtcgtgagttcgtta	1117
Oy	657	TGGGGAAGATTATGATCTCAGACACAGAGGTTCTTCACATGATCCTCTGCACACAGT	716
Dh	1118	tgcgagagacattgagatttcaagaccagagagcttcccaagatccctgtcagcaagt	1177
Oy	717	CAAAAAGCTCAAGGGGATGACGTGGGGAATCACTCTTGCCAGTTTGACAGATATGGC	776
Dh	1178	caaaaagctgaagggagatgagtgtgcgatactcttgcgagcttgcacagataatgac	1237
Oy	777	AGCAAAAGCTTCTTGTGCTTCGAGGAGGAGCATGTTTGGGCAAGTACCAAGTGAT	836
Dh	1238	agcaaaagtgttcctgtgtgtcatctcagagagaaatgtatgtatgaataatcatcgtgatt	1297
Oy	837	CATCCCGGAGATGTATCGAGCCTGCGTGTGTGGAGACAGTGCATGTGGAGGCCAATTCTCT	896
Dh	1298	catctccgagctgtacacgacctctctgtgtgagagaggttgacacgaaacccaactcaac	1357
Oy	897	ACGCTCCCTGCCCACAAACCCTCCTGGGTGCATGGAAGTTACATCCGAATGTGACTTTGA	956
Dh	1358	ccgctgcctccggaagaattctgtctgtgctcagtgaagggtctacatctgctgtgattctga	1417
Oy	957	GCCCCGACCTCCCAACAAATCAAGACACATCTCAGGAAAGCTCCACAGAGTATTAAG	1016
Dh	1418	gcccctcgagcttccaagacgaataagacacatctcaagaaagctccacaagacgatacagag	1477
Oy	1017	AGAGTCAACACAGCAAAAGCTTACAGCGTGGGGGCCAGCAAGTTCCATGGGTACGCTACGA	1076
Dh	1478	agagttcaacaacaacagcggtcaagcgctgtgagggcccaagtaagttlccacggtatccataga	1537
Oy	1077	TGGGATCTGGGTATCATCGCCAGAACCCCTACAGAGAGGCGCATGAGCACTGCATCCGATG	1136
Dh	1538	tgtgactctgtgtcatcgcgcaagaacactgcagaggggacatgtgagacactgtatgccaag	1597
Oy	1137	CAGGCACAGCGGATTCAGGACTTCAACTACACAGACACACGCTGGGGCAAAATCATCTCT	1196
Dh	1598	ccgcaacacagcggtaccgagacttcaactacacagagccacacgccttgggcagagctacctc	1657
Oy	1197	CAATGCCATGAACGAGACCAACTTCTTCGGGGTCACGGGGTCAAGTTGTGTTCCGGAACG	1256
Dh	1658	caatgcacatgaacagagaccactcttcttcgggtgcacggtcaadtgtatcttcgagatg	1717
Oy	1257	GGAGAGATGGGACCAATTAATTACTCAATTCAAGACAGCAAGAAAGGTGAAGGTCCG	1316
Dh	1718	ggagagagatgggagacctaatattactcaatttcaagacagcgagggttgaaggttgg	1777
Oy	1317	CGAATCAACGCGGTGCTGACACATCTGAGATCATCATATGACACATAAGTTTCCAGGG	1376
Dh	1778	agagttcaaaagctgtgtgcgcgaacaacgtgagatcatalgacacactcaggttccaaag	1837



Dd 698 gtggaactgcccacatcgagcagatccgcgaagcagatccctcgcgcctactcctcagac 757  
Qy 298 CTGGACTATGACACCGAGTGTGACAAATGCAAGAGACTGAAGCCCTTCTATGACGA 357  
Dd 758 ctgcgctctatgacacgagtgatgcgaacgaagaggttgaagccttcttaagatgca 817  
Qy 358 ATAAAGTATGGCGCAACCTTGTATGAGTGTGAGAGCGCTGTGCGTGTGACATCT 417  
Dd 818 ataaataacagggccgaacccacttgatggtgttgagagcgctgtctccatccgttacc 877  
Qy 418 ATATCGCGAGTCCCTCCAAAGGCTGGAATCTGTGACAGCTTTCCTTGCCTGACCAAG 477  
Dd 878 atccttgacagatccctccaaagcgtggaatcgtgacagcttcttcttgccgaacacg 937  
Qy 478 CCGTCTTTCGCGATAGAAGATACCGGTATTTCTTCGAGAGGCTGCGTCAAGCAAC 537  
Dd 938 cctgtctacgagtaagaaaaataccttacttcttcttggaacgctccatccacgaacat 997  
Qy 538 GCGGTGAACCCCGCATCTCTGAAGCTCTGAAGACACTTCCGCTGGCGGCTGTGGCACA 597  
Dd 998 gctgtgataccagccactctgaagtgtctcaagcactcaccagtggaagcgctgagcag 1057  
Qy 598 CTCACGAGGAGCGTGCAGCGCTTCTCCGAGTGAAGAAATGACCTGACCTGCGGTCTGTAT 657  
Dd 1058 ctgcagcaagaagcgttcagaggtctctcgtgaggtgcggaatgacctgacgttgctctat 1117  
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Qy 778 GCAAAATCTTCTGTTGTTGCTTCTGAGAGAGATGTTGCGACAAATATACATGAGATC 837  
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Qy 1258 GAGAAATGGAACCATTAATTTACTCAATTTCAAGACAGCAGAGAGTGAAGTCCGC 1317  
Dd 1718 gagagaatggtgacatlaaattactcaattcgaagcagcaggtgtaaggtgga 1777  
Qy 1318 GAATTCACGCGGTGCTGACACACTGAGATCATCAATGAACCATTAAGTGTCCAGGCG 1377  
Dd 1778 gagtacaacgctgtggtcagacacatcgtgagatcaatcaatgacacatcaaggttccaaga 1837

Qy 1378 TCGAGCCACCCAAAGCAACGACATCTTCTGAGACAGCTTGGAAAGATCTCGCTTCCA 1437  
Dd 1838 tccgaaccacacaaagacaaagacacatcctcgtgagagcgtgcggaagatcctcactac 1897  
Qy 1438 CTGTATGACATCTGTGCCCTCTCACACATCTCTGCGGATGATCATGAGCGGCTTCTC 1497  
Dd 1898 ctctacagatcctctctcctcctcactcctcgtgagatgacatcagcaggtcttctcc 1957  
Qy 1498 TTCTTCAACATCAAGAACCGGAAACCAAAAGCTGATTAAGATGTCAAGCCCTCATGAAC 1557  
Dd 1958 ttcttcaacatcaagaacccggaatcaagaagctcaaaagtctgagatccatcaatgaac 2017  
Qy 1558 AACCTCATCTCTGGGAGGAATGCTGTCTATGATCATCACTTCTCTTGGCTCGAT 1617  
Dd 2018 aacctatcctcttgtaggagatgctcctcctatgcttccatattctcttcttgccagat 2077  
Qy 1618 GGGTCTTCTCTCAAAAAGACCTTGAACACTCTGCAAGGTCGCGGACCTGGATTTCTC 1677  
Dd 2078 ggaaccttgctctgaaaaagacacttgaaaacacttgacacgctcagagctgattctc 2137  
Qy 1678 ACCGTGGGCTACCAACTCCTTGTGGGCGCATGTTTGCAAAAGACTGTGAGGTCATGCG 1737  
Dd 2138 accgtgggtacacgacgcgcttggggccatgtttgcaagacctgagagatccacgcgc 2197  
Qy 1738 ATCTTCAAAAATGTAAGATGAAGAAGATCATCAAAAGCCGAAGCGCTTGTGATTT 1797  
Dd 2198 attctcaaaaatgtaaaatgaaagaagatcaacaaagacaaacatcgtctgtgac 2257  
Qy 1798 GTGGGGGCTGCTGCTCATCGACCTGTGCATCTGATCTGTGTCAGAGCTGTGACCCC 1857  
Dd 2258 gtgggggctatgctctgtatcgaacctgtgtatcgtatcgtctgagctggtgagacccc 2317  
Qy 1858 CTGCGGAGGACATAGAGAGTACAGCATGAGCGCGGACCGACGCGGACATCTCC 1917  
Dd 2318 ctgcgaagagacagtgagaagatgacagcatcagacgacccagagagacggtatctcc 2377  
Qy 1918 ATCCGCCATTTGCTGGAACACTGCGAAAACCCACATGACCATCTGTGCTTGGCTTGTG 1977  
Dd 2378 attccgctctctctgagacactgtgaaacacacatagacatctgtctgacatcgtc 2437  
Qy 1978 TACGCTTCAAGGGGCTCTCATGCTATCGGTTGTTCTTGGCATGGAAACCGCAT 2037  
Dd 2438 tatgctcaaaaggaacttctcatgtgtcgtgtgtcttcttgaagcttgaggaccggac 2497  
Qy 2038 GTGAGCATCTCTGCTCTCAACGACGACGAAGTACATCGGCATGATGTGTACATGTGG 2097  
Dd 2498 gtccagcatcccgcaactcaacgacagcaagatcatcgtgagtggtctcaacagtgg 2557  
Qy 2098 ATCATGTGATCATCGGGGCTGTGCTCTCTCTGACGCGTGTGACAGCCAAAGTGTGAC 2157  
Dd 2558 atcatgtcatctatcgtggcgctgtctctctcctcgtacccggacagcccaatgtgag 2617  
Qy 2158 TTCTGCACTGTGGCCTGCTGATCATCTTCTGTGACACCATCATCTCTGCTGTGT 2217  
Dd 2618 ttctgcatcgtgtcgtcgtgtcatcactcctcgtcagcacacacacccctcgtgatac 2677  
Qy 2218 GTGCAAGGCTCATTTACTGTGAGGACAAACCTTGACGAGCAGCTGTGAGAACAGGCGTTC 2277  
Dd 2678 gtgcgaagctctcatccctcgtgaaacaaacccagatgacgaacagcagaagcgtctc 2737  
Qy 2278 CAGTTACACGAGAACGAGAAGAAAGATTGTGAGACACTCTCTCATGACACAGCGT 2337  
Dd 2738 cagttcactcaagaatcagaagaagaatctctaaacgtctccactcgtccacagtggt 2797  
Qy 2338 AACGAGCGAGACGTCCAGCCTGAGGAGCTGTGAGTGAAGAAACACCGCTTGAATG 2397  
Dd 2798 aaccaagccagacatcccgctgagggcctacagtcagaanaacatcgcctgagatg 2857  
Qy 2398 AAGATTCACAGAGGTGGCAAGACTGTGAAGAAAGTACCATGTGAGCTGTGACAGACACA 2457  
Dd 2858 aagatcacagagctgtgataaagacttgaaaggtctacacatgacgctcgtcgtgacacaca 2517







GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: March 16, 2000, 11:46:08 ; Search time 1755.56 Seconds  
(without alignments)  
6071.396 Million cell updates/sec

Title: US-09-211-755-3  
Perfect score: 2823  
Sequence: 1 ATGGCTTCCCGCCGAGATC.....TCATGCTTCGCGGCGCTGTAG 2823

Scoring table: IDENTITY\_NTC

Searched: 4538634 seqs, 1887831982 residues

Database : EST:\*

Word size : 0

Number of hits that pass the threshold : 9077268

1: em\_est1:\*  
2: em\_est2:\*  
3: em\_est3:\*  
4: em\_est4:\*  
5: em\_est5:\*  
6: em\_est6:\*  
7: em\_est7:\*  
8: em\_est8:\*  
9: em\_est9:\*  
10: em\_est10:\*  
11: em\_est11:\*  
12: em\_est12:\*  
13: em\_est13:\*  
14: em\_est14:\*  
15: em\_est15:\*  
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19: em\_est19:\*  
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22: em\_est22:\*  
23: em\_est23:\*  
24: em\_est24:\*  
25: em\_est25:\*  
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27: em\_est27:\*  
28: em\_est28:\*  
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50: gb\_est31:\*  
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52: gb\_est33:\*  
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54: gb\_est35:\*  
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98: gb\_est79:\*  
99: gb\_est80:\*  
100: gb\_est81:\*  
101: gb\_est82:\*  
102: gb\_est83:\*  
103: gb\_est84:\*  
104: gb\_est85:\*  
105: gb\_est86:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	345	12.2	397	43	A1214087 ap29g06.x
2	304.2	10.8	704	63	A1968032 w12c11.x
3	293.2	10.4	371	22	H14151 ym62d04.r1
4	257.4	9.1	341	20	Z43654 HSC1H041.n
5	230.6	8.2	560	45	A1341249 qx90d04.x
6	203.6	7.2	368	20	T07621 EST05511.Fe
7	202.8	7.2	853	87	A0744524 HS_5508_A

RESULT	ALIGNMENTS
1	
AI214087	
LOCUS	
DEFINITION	AI214087 397 bp mRNA EST 21-OCT-1998
ACCESSION	ap29g06.x1 Schaller astrocytoma Homo sapiens cDNA clone
VERSION	IMAGE:1958826 3 similar to tr:008621.008621 GABA-B1B1 RECEPTOR. ;
KEYWORDS	mRNA sequence.
SOURCE	AI214087 AI214087.1 GI:3777668
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
TITLE	1 (bases 1 to 397)
JOURNAL	Hillier, L., Allen, M., Bowles, L., Dubnue, T., Geisel, G., Jost, S.,
COMMENT	Kritzman, D., Kneuba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
	Martin, J., Moore, B., Schellenberg, K., Stepec, M., Tan, F.,
	Theising, B., White, I., Wylie, T., Waterston, R., and Wilson, R.
	Unpublished (1997)
	On Jan 17, 1998 this sequence version replaced gi:1900223.
	Contact: Wilson RK
	Washington University School of Medicine
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
	Tel: 314 286 1800
	Fax: 314 286 1810
	Email: est@watson.wustl.edu
	This clone is available royalty-free through INLTL; contact the
	IMAGE Consortium (info@image.llnl.gov) for further information.
	Possible reversed clone: similarity on wrong strand

FEATURES					
Source					
	1..397	/organism="Homo sapiens"			
		/db_xref="taxon:9606"			
		/clone="IMAGE:1956826"			
		/clone_1ib="Schiller astrocytoma"			
		/sex="male"			
		/issue_type="astrocytoma"			
		/dev_stage="44 years"			
		/lab_host="SOLR"			
		/note="Organ: brain; Vector: pBluescript SK- (Stratagene))"; site_1: EcoRI; Site_2: XhoI; Double-stranded cDNA was prepared from human astrocytoma using primer 5'-GAGAGAAGAGAGAGAGAAATACGTAG(18)-3'. An EcoRI adaptor was used on the 5' end of the cDNA as follows: 5'-AATTCGGCAGCG-3'. The library was size-selected and went through one round of amplification. Average insert size is 1.7 kb, with a range from 0.4-12 kb. Tumor identification by consensus pathology. This library was constructed by Dr. Martin Schiller (Johns Hopkins University)."			
BASE COUNT	109 a	109 c	115 g	64 t	
ORIGIN					
Query Match	12.2%	Score 345;	DB 43;	Length 397;	
Best Local Similarity	92.4%;	Pred. No. 9,2e-56;			
Matches 363;	Conservative 0;	Mismatches 30;	Indels 0;	Gaps 0;	
OY 1030	AAACGTTCAAGCTGGGGGCCACAGCAAGTCCATGGGTACGCCTCATGATGGATCTGGGTC				1089
Dd 5	AAGCGTGACGGCTGGGGGCCACGAAGTCCACGGGTACGCTACGATGGCATCTGGGTC				64
OY 1090	ATGCCCAAGACCCTTAAGAGGGCCATGAGACACATCGCATGTCATACGACGACCCAGCGG				1149
Dd 65	ATGCCCAAGACTCGAGAGGGCCATGAGACATCGCATGTCACACACCCGACACAGCGG				124
OY 1150	ATCCAGACTTCACTACACAGACACAACGGCTGGGCAAAATCATCTCAATGGCATGAAC				1209
Dd 125	ATCCAGACTTCACTACACAGACACAACGGCTGGGCAAGATCATCTCAATGGCATGAAC				184
OY 1210	GAGACCAACTCTTCGGGGGTCAAGGTCGAAGTGTGTCCGGAACGGGGAGAGATGGGA				1269
Dd 185	GAGACCAACTCTTCGGGGGTCAAGGTCGAAGTGTGTCCGGAATGGGGAGAGATGGGG				244
OY 1270	ACCATTAATTACTCAATTTCAAGACACAGAGAGGTGAAGTTCGGCCAATCAACCGG				1329
Dd 245	ACCATTAATTACTCAATTTCAAGACACAGAGAGGTGAAGTTCGGCCAATCAACCGCT				304
OY 1330	GTGGCTGACACACTGGAGATCATCATATACACCAATTAAGTTCACAGGGGTCCGAGCCACC				1389
Dd 305	GTGGCTGACACACTGGAGATCATCATATACACCAATTAAGTTCACAGGGGTCCGAGCCACC				364
OY 1390	AAGGACAAGACATCATCTTCTGGAGAGGCTGGG				1422
Dd 365	AAAGCAAGACATCATCTTCTGGAGAGGCTGGG				397
RESULT 2	AI968032/c				
LOCUS	AI968032	704 bp	mRNA	EST	25-AUG-1999
DEFINITION	w112c11.x1 NCL_CAP_G66 Homo sapiens cDNA clone IMAGE:2516756				3'
	similar to TR-075975 075975 GABA-B RECEPTOR SPLICED VARIANT 2 ;,				
	mRNA sequence.				
ACCESSION	AI968032				
VERSION	AI968032.1	GI:5764850			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				











\_\_\_\_\_



KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM *Mus musculus*.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 512)  
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
TITLE Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)  
JOURNAL MEDLINE  
COMMENT 97044477  
On Mar 16, 1998 this sequence version replaced gi:2961822.

FEATURES	Location/Qualifiers
source	1. .512

BASE COUNT	121 a	132 c	133 g	126 t
ORIGIN				

Query Match	3.68;	Score 102.2;	DB 64;	Length 512;
Best Local Similarity	57.8%;	Pred. No. 7.5e-10;		
Matches 182; Conservative	0;	Mismatches 133;	Indels 0;	Gaps 0

Qy	1989	GGGGCTCTCATGCTATTTCGTTTCTTCTTGCGATGGGAAACCCGCAGATGTGACATCCC	2048
Db	451	AGGGCTGGTGGCTGGCGGGAATCTTTCGTATATGAACCCAAAGTGTCCACTGA	392
Qy	2049	TGCGCTCAACGACAGCAAGTACATCGGCATAGTGTATACATGTGGGCATCATGCAAT	2108
Db	391	AAAGATCAATGATCCACAGAGCGCGTGGGAGTGGCTATACAAATGTTGGCGTCTGATCT	332
Qy	2109	CATCGGGGCTGCTCTCTTCTCTGACGCGTGAACCAAGTCAGTTCTGCATCGT	2168

Db 331 CATTACCGCTCTCCGTGACCATATCTCTTCCAGCGCCAGGACGGACCACTTCGCTTTGG 212

Qy 2169 GGCCTCGTATATCTCTTGAGCAGCATCACTCTCGCTCGTGTGTTTGGCAAAAGT 2228

Db 271 CTCCTGGCCATGTGTCCTCTTCCATTACTCTGCTGTGCTCTTGGCTAGAT 212

Qy 2229 CATTACTCTAGAGC 2243

Db 211 GCGCAGGTATATCAC 197

RESULT	14	
AM158263		
LOCUS	393 bp	05-NOV-1999
DEFINITION	EST	
	2339908.x1 Xenopus laevis	CDNA clone za39b00
ACCESSION	5', mRNA sequence.	
VERSION	AM158263	
KEYWORDS	AM158263.1	GI:6270292
SOURCE	EST	
ORGANISM	African clawed frog.	
	Xenopus laevis	

TITLE	Expressed sequence tags from <i>Xenopus</i>
JOURNAL	Unpublished (1999)
COMMENT	On May 18, 1998 this sequence version replaced gi:3137122

BASE COUNT	94 a	98 c	91 g	110 t
ORIGIN				

Query Match	3.4%;	Score 95.4;	DB 71;	Length 393;
Best Local Similarity	54.8%;	Pred. No. 1.3e-08;		
Matches 189;	Conservative	0;	Mismatches 156;	Indels 0;
			Gaps	0

QY	1808	TGCTTCATGACCTGACCTGCATCCTGATCTGTGTGGAGGCTGTGGACCCCCCTCCGGAGA	1867
Db	31	TGCTGGCCCTGATSTCAATACACTAGGATCTGGCAATAGTGGACCCCCCTCAAGCTT	90
QY	1868	CAGTAGAGAGGTACGATGAGTGGACGCCGAGACCCAGAGCCGGGACATCTTCATCCGCCAT	1927
Db	91	CTATTGAGGAATTTACCAAAAGAAACACCTGCTGATGACCTGGATGTTCTCAATACCTCCGC	150
QY	1928	TGCTGGACACTGGGAAACACCCACATGACCATCTGGCTGGCATGTCTACGGCTACA	1987

Db 151 AGCTGGAACACTGCTACCTTCTCTCAAGATGAACACATGCGCTGTATAGTATAGGCTCTA 210  
 QY 1988 AGGGGCTCCTCATGCTATTTCGGTGTCTTCTTGCGATGGAAACCCGCATGTGAGCATCC 2047  
 Db 211 AAGGGCTACTCTTCTTGGCTGTATATCTTGGCTATAGAACCAAGAGTTCACACG 270  
 QY 2048 CTGGCTCAACGACAGCAAGTACATCGCAATGAGTGTACATATGAGGAGTCAATGCA 2107  
 Db 271 AGAAGATCATATGACACACCGTGTGTGGGATGGCATATATACATGTGGCTGTCTTGGC 330  
 QY 2108 TCATCGGGGCTGCTGTCTCTTCTGACCGCTGACCAAGCCACG 2152  
 Db 331 TCATCACCGCTCCAGTACATGATCTCAGTACGACAGCAGC 375

## RESULT 15

AA567648

LOCUS AA567648 404 bp mRNA EST 28-NOV-1998  
 DEFINITION HL01578: 5prime HL Drosophila melanogaster head Bluescript

ACCESSION AA567648  
 VERSION AA567648.1 GI:2340430

KEYWORDS EST.  
 SOURCE fruit fly.

## ORGANISM

Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

## REFERENCE

1 (bases 1 to 404)  
 Harvey, D., Hong, L., Evans-Holm, M., Pendleton, J., Su, C.,  
 Brokstein, P., Lewis, S. and Rubin, G.M.  
 BDGP/HMI Drosophila EST Project  
 Unpublished (1997)  
 On Sep 12, 1996 this sequence version replaced gi:1394839.  
 Contact: Harvey, D.

## TITLE

JOURNAL

COMMENT

G. M. Rubin-Molecular and Cell Biology  
 University of California Berkeley  
 539 USA, Berkeley, CA 94720-3200, USA  
 Fax: 510 643 9947  
 Email: [http://www.fruitfly.org/EST\\_est@fruitfly.berkeley.edu](http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu)  
 Plate: 15 row: G column: 6  
 High quality sequence stop: 379.  
 Location/Qualifiers

## FEATURES

source

1..404  
 /organism="Drosophila melanogaster"  
 /db\_xref="BDGP\_EST:BDc1n022505"  
 /db\_xref="taxon:7227"  
 /clone="HL01578"  
 /clone\_1ib="HL Drosophila melanogaster head Bluescript"  
 /sex="male and female"  
 /dev\_stage="adult"  
 /lab\_host="SOLR"  
 /note="Organ: head-Brain & sensory organ; Vector:  
 Bluescript SK; Site\_1: EcoRI; Site\_2: XhoI; Constructed  
 using Stratagene ZAP-cDNA Synthesis kit. Oligo dt-primed  
 and directionally cloned at EcoRI and XhoI in Bluescript  
 SK(+/-)"

BASE COUNT 105 a 90 c 88 g 121 t  
 ORIGIN

Query Match 3.3%; Score 94.2; DB 35; Length 404;  
 Best Local Similarity 54.9%; Pred No. 2.3e-08;  
 Matches 186; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

QY 1374 GGGGTCGAGCCACCAAGACATCTTCTGAGCAGCTTCGGAAGATCTCGCT 1433  
 Db 66 GGGGAAAACCTCCCAAGATCGCACTTGTATCTACATCGACAGTCAAGTCAATCC 125  
 QY 1434 TCACATGTATGATCTGCTGCTCTACATCTCTGCGATGATCATGCGACAGCGCTT 1493  
 Db 126 AACCATATATATGTATCGGCTAGTCTCGTCTCATGTGAGTATATTCGACAGTTT 185

QY 1494 CCTCTTCTTCAACATCAAGAACCGGAACCAAGCTGATTAAGATGTCAAGCCCTACAT 1553  
 Db 186 TCTGGCTTTTAACTTAAGTATCGCAATCAAGATCAAGATGTCAAGTCCCATTT 245  
 QY 1554 GAACAACTCATATCTCTGAGAGAAATGCTGCTATGATCATCTCTCTTTGGCT 1613  
 Db 246 GAACAACTCATATGAGGCTGTATGATGATGATGATGATGATGATGATGATGATGAT 305  
 QY 1614 CGATGGGTCTTCTGCTCAAGAAAAGACCTTTGAAACACTCTGACAGTCCGAGCTGGAT 1673  
 Db 306 CGATACCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 365  
 QY 1674 TCTCACGCTGAGCTACACAACTGCTTTGGGGCCATGT 1712  
 Db 366 CTGATGCTGAGTCAATCAATCTCAATTTTGGAGCCATGT 404

Search completed: March 16, 2000, 11:46:20  
 Job time: 1887 sec



(TM)

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Mpsrch_pp    protein - protein database search, using Smith-Waterman algorithm
Run on:      Wed Mar 15 22:13:59 2000;      MasPar time 99.69 Seconds
Tabular output not generated.              653.763 Million cell updates/sec

```

Title:	>US-09-211-755-4
Description:	(1-940) from US09211755.pep
Perfect Score:	6906
Sequence:	1 MASPPSSQPPPPPPPPA.....TASRRHHVPPSRVMSGL 940

Scoring table: PAM 150

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 08  
Listing first 45 summaries

Database:

1:sp\_aarchaea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human  
5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle  
9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified  
13:sp\_vertebrate 14:sp\_virus

Statistics: Mean 54.925; Variance 104.973; scale 0.523

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description	Pred. No.
1	6894	99.8	940	11	088871	GABA-B RECEPTOR GB2.	0.00+00
2	6772	98.1	941	4	075899	GABA-B RECEPTOR.	0.00+00
3	2234	32.3	1221	5	09Y133	BCDNA.GH07312.	0.00+00
4	1684	24.4	844	4	096022	GABAB RECEPTOR, SUBUNIT	0.00+00
5	1680	24.3	812	11	092308	GABAB RECEPTOR 1D.	0.00+00
6	1681	24.3	833	11	09WV15	573K1.1.4 (GAMMA-AMINO	0.00+00
7	1681	24.3	844	11	09WV17	573K1.1.2 (GAMMA-AMINO	0.00+00
8	1680	24.3	844	11	008621	GABA-BR1 RECEPTOR.	0.00+00
9	1676	24.3	899	4	095975	GABAB RECEPTOR, SUBUNIT	0.00+00
10	1671	24.3	930	4	095375	GABA-B1A RECEPTOR.	0.00+00
11	1676	24.2	961	4	095468	GABAB1 PROTEIN.	0.00+00
12	1673	24.2	960	11	09WV20	573K1.1.1 (GAMMA-AMINO	0.00+00
13	1672	24.2	960	11	008620	GABA-BR1A RECEPTOR.	0.00+00
14	1671	24.2	960	11	09WV28	GABA-B1A RECEPTOR.	0.00+00
15	1346	19.5	211	11	075975	GABA-B1A RECEPTOR.	0.00+00
16	1350	19.5	662	11	09WV16	573K1.1.3 (GAMMA-AMINO	0.00+00
17	1349	19.5	875	11	092609	GABAB RECEPTOR 1C.	0.00+00
18	1341	19.4	891	11	092604	GABAB RECEPTOR SUBTYPE	0.00+00
19	1163	16.8	102	4	075974	GABA-B RECEPTOR SPLIC	1.68e-11
20	720	10.4	482	5	Q23442	CSM2D KX180.	1.34e-116

21	495	7.2	528	5	096954	METABOTROPIC GLUTAMATE
22	252	3.6	953	10	092657	POTATIVE ION CHANNEL P
23	231	3.3	908	4	095945	METABOTROPIC GLUTAMATE
24	211	3.1	253	5	092343	COMSD 2K180
25	217	3.1	923	10	092768	POTATIVE ION CHANNEL P
26	216	3.1	940	10	081078	POTATIVE LIGAND-GATED
27	212	3.1	983	11	082916	METABOTROPIC GLUTAMATE
28	197	2.9	868	13	073636	PHEROMONE RECEPTOR.
29	202	2.8	962	10	023048	SIMILAR TO ARABIDOPSIS
30	190	2.8	898	10	081776	HYPOHETICAL 9.9 K D P
31	194	2.8	1151	13	09M616	GUANYLATE CYCLASE OGC
32	190	2.8	1287	5	093564	FA5H1.1 PROTEIN.
33	184	2.7	1151	13	083335	MEMBRANE GLYNTLY CYCL
34	179	2.6	501	4	095946	METABOTROPIC GLUTAMATE
35	181	2.6	779	11	055269	POTATIVE PHEROMONE REC
36	180	2.6	864	13	073637	PHEROMONE RECEPTOR.
37	177	2.5	940	13	073638	CALCUM2+ SENSING RECE
38	170	2.5	856	13	073639	PHEROMONE RECEPTOR.
39	173	2.5	912	11	070410	POTATIVE PHEROMONE REC
40	164	2.4	848	13	093553	POTATIVE OODRANT REECP
41	167	2.4	855	13	073640	PHEROMONE RECEPTOR.
42	165	2.4	1135	5	021669	GUANYL CYCLASE PRECURS
43	160	2.3	161	13	073643	METABOTROPIC GLUTAMATE
44	161	2.3	840	11	092088	POTATIVE TASTE RECEPTO
45	158	2.3	844	13	093552	POTATIVE OODRANT REECP

## ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT:	940 AA.
ID	088871			
AC	088871;			
DT	01-NOV-1998 (TREMBLrel. 08, Created)			
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)			
DT	01-MAY-1999 (TREMBLrel. 10, Last annotation update)			
DE	GABA-B RECEPTOR GB2.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia			
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
RN	[1]			
RC	SEQUENCE FROM N. A.			
RC	TISSUE=CEREBRAL CORTEX;			
RA	CLARK J.C., LAM A., BONNER T.I.;			
RT	"gb2, A second GABA-B receptor".			
RL	Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: A058795; AAC63994.1; .			
DR	PFAM: PF00003; Tm3.3.1			
DR	PFAM: PF01094; ANF_Receptor; 1.			
DR	SEQUENCE 940 AA; 105762 MW; 94C8C3C1 CRC32;			

Query Match	99.88;	Score 6894;	DB 11;	Length 940;
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Best local similarity	99.86	Pred.No. 0.00e+00
Matches	938	Conservative 1; Mismatches 1; Indels 0; Gaps 0

Db	1	MASPPSSGQPPPPPPPPARLLRLLLSLMLABGAMGTGCAAPPSPSSPISIMGL	60
Qy	1	MASPPSSGQPPPPPPPPARLLRLLLSLMLABGAMGTGCAAPPSPSSPISIMGL	60
Db	61	MPUTEVAKSGIGRGVLPVAVELAIEOIRNESLLRPFLIDRLRYTECDNNAKGLKAFYTAI	120
Qy	61	MPUTEVAKSGIGRGVLPVAVELAIEOIRNESLLRPFLIDRLRYTECDNNAKGLKAFYTAI	120
Db	121	KGPPHMLVFGGVCPSVSTSI <sup>1</sup> IAESIQGMNVLVSFAATT <sup>2</sup> PVLADKKR <sup>3</sup> PYFEFTYPSDNA	180
Qy	121	KGPPHMLVFGGVCPSVSTSI <sup>1</sup> IAESIQGMNVLVSFAATT <sup>2</sup> PVLADKKR <sup>3</sup> PYFEFTYPSDNA	180
Db	181	VNPATILKLKLFHFRMRVGTLLTDQXRFSEVRNDLTGVLGEDIEISDTESFSNDPCTSYK	240
Qy	181	VNPATILKLKLFHFRMRVGTLLTDQXRFSEVRNDLTGVLGEDIEISDTESFSNDPCTSYK	240
Db	241	KLGKNDVRIILGQFDONMAKAVFCCAEESMFGSKYQWILGQWEPAMQVHVEANSR	300
Qy	241	KLGKNDVRIILGQFDONMAKAVFCCAEESMFGSKYQWILGQWEPAMQVHVEANSR	300

Db 301 CLRSLLAAMEGYIGVDEPLSSKOIKTISKTPQOEREYKRSQVPSKFGHAYDG 360  
 Qy 301 CLRSLLAAMEGYIGVDEPLSSKOIKTISKTPQOEREYKRSQVPSKFGHAYDG 360  
 Db 361 IWTIAKTLOPAMETLHASSRHORIODENYDHTLGLKILNANMETFEVYGOVFRNGE 420  
 Qy 361 IWTIAKTLOPAMETLHASSRHORIODENYDHTLGLKILNANMETFEVYGOVFRNGE 420  
 Db 421 RMGIFKTFQPODSREYKVEYNAVADTLEIINDTIRQSGSEPPKDTIILEQLKISLPL 480  
 Qy 421 RMGIFKTFQPODSREYKVEYNAVADTLEIINDTIRQSGSEPPKDTIILEQLKISLPL 480  
 Db 481 YSILSALTILGIMTASAFLEFNIRNOKLIKMSPPYNNLILGMLSYASTIFLFGIDG 540  
 Qy 481 YSILSALTILGIMTASAFLEFNIRNOKLIKMSPPYNNLILGMLSYASTIFLFGIDG 540  
 Db 541 SFVSEKTEFTLCTVTRTWILTVGYTTAFSGAMFAKTWRVHAIFKNVKKKKIINDOKLLVTV 600  
 Qy 541 SFVSEKTEFTLCTVTRTWILTVGYTTAFSGAMFAKTWRVHAIFKNVKKKKIINDOKLLVTV 600  
 Db 601 GGMILIDCLICQWAVDPLRTRVERYSMEPPDPAGRDISIRPLEGENTHMTWLTGLTV 660  
 Qy 601 GGMILIDCLICQWAVDPLRTRVERYSMEPPDPAGRDISIRPLEGENTHMTWLTGLTV 660  
 Db 661 AYKGLMLFEGCFIAMETRVNSIPALNDSKYIGMSYVNGIMCIIGAASFILRDOPNVOF 720  
 Qy 661 AYKGLMLFEGCFIAMETRVNSIPALNDSKYIGMSYVNGIMCIIGAASFILRDOPNVOF 720  
 Db 721 CIYALVLIIFCSTITLCLVFPRLITLKNPDAONRFOFTONOKKEDSKTSTVTSYN 780  
 Qy 721 CIYALVLIIFCSTITLCLVFPRLITLKNPDAONRFOFTONOKKEDSKTSTVTSYN 780  
 Db 781 QASTSRLEGQSNHRLRKITELDKLEBYTMOLODPRETTYIKONHGOELNDLSIG 840  
 Qy 781 QASTSRLEGQSNHRLRKITELDKLEBYTMOLODPRETTYIKONHGOELNDLSIG 840  
 Db 841 NFIYSTDGGKAILKNHLDONPOLQNTTPEPRTCKDPLEDINSEHIOQLSLQPLIHH 900  
 Qy 841 NFIYSTDGGKAILKNHLDONPOLQNTTPEPRTCKDPLEDINSEHIOQLSLQPLIHH 900  
 Db 901 AYLPISIGVDASCVSPSPASPRHRHVPPSPFRVMSGL 940  
 Qy 901 AYLPISIGVDASCVSPSPASPRHRHVPPSPFRVMSGL 940  
 RESULT 2  
 ID 075899 PRELIMINARY: PRT: 941 AA.  
 AC 075899:  
 DT 01-NOV-1998 (TEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)  
 DT 01-MAY-1999 (TEMBLrel. 10, Last annotation update)  
 DE GABA-B RECEPTOR.  
 GN GABAB-R2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RA CLARK J.C., LAM A., BONNER T.I.;  
 RT "902, a second GABA-B receptor";  
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-CEREBELLUM;  
 RA WHITE J.H., WISE A., MAIN M.J., GREEN A., FRASER N.J., DISNEY G.H.,  
 RA BARNES A.A., EASON P., FOORD S.M., MARSHALL F.H.;  
 RT "Heterodimerisation is required to form a functional GABAB receptor.",  
 RL Submitted (OCT-1998) to EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-HIPOCAMPUS;

RA BOROWSKY B., LAZ T., GERALD C.;  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-HIPOCAMPUS;  
 RA BOROWSKY B., LAZ T., GERALD C.;  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF056085; AAC63228.1; -  
 DR EMBL; AJ012188; CA09942.1; -  
 DR EMBL; AF074483; AAD03336.1; -  
 DR PFM; PF00003; 7tm.3; 1.  
 DR PFM; PF01094; ANF\_receptor; 1.  
 KW Signal; Receptor  
 SQ SEQUENCE 941 AA: 105821 MW: 83821 DALY CRC32;  
 Query Match 98.18; Score 6772; DB 4; Length 941;  
 Best Local Similarity 97.88; Pred. No. 0.00e+00;  
 Matches 920; Conservative 15; Mismatches 5; Indels 1; Gaps 1;  
 Db 1 MASRSSGQGPPEPPPPARLLLLPLLLPLPLAGAMGAMGAPRPPSSPISMG 60  
 Qy 1 MASPPSSGQP-REPPPPPARLLPLLLSLLMLAGAMGWTGAPRPPSSPLSING 59  
 Db 61 LMPLEKVAAGSISGRVLAVALAEIQRNESLRRPFLDLRLYDTEONAKLAFYTA 120  
 Qy 61 LMPLEKVAAGSISGRVLAVALAEIQRNESLRRPFLDLRLYDTEONAKLAFYTA 119  
 Db 121 IKYPNHLMWFGVCPDVSYSIAESLQGMNLVOLSFATTPVLADKKKYPYFRTVPSDN 180  
 Qy 120 IKYPNHLMWFGVCPDVSYSIAESLQGMNLVOLSFATTPVLADKKKYPYFRTVPSDN 179  
 Db 181 AVNPAIILKLKHOMKRVGLTQDOVRFSEVRNDLTGLYGEDIEIDTSPSNDPCTSV 240  
 Qy 180 AVNPAIILKLKHOMKRVGLTQDOVRFSEVRNDLTGLYGEDIEIDTSPSNDPCTSV 239  
 Db 241 KKLGNQVRIILQFQNNAAVFCGAYEEMNGSKTOMIIPGYPESSWEQYHTFANS 300  
 Qy 240 KKLGNQVRIILQFQNNAAVFCGAYEEMNGSKTOMIIPGYPESSWEQYHTFANS 299  
 Db 301 FCLRNKLLAAMEGYIGVDEPLSSKOIKTISKTPQOEREYKRSQVPSKFGHAYDG 360  
 Qy 300 FCLRNKLLAAMEGYIGVDEPLSSKOIKTISKTPQOEREYKRSQVPSKFGHAYDG 359  
 Db 361 GIWIAKTLOPAMETLHASSRHORIODENYDHTLGLKILNANMETFEVYGOVFRNGE 420  
 Qy 360 GIWIAKTLOPAMETLHASSRHORIODENYDHTLGLKILNANMETFEVYGOVFRNGE 419  
 Db 421 ERMGITKTFQPODSREYKVEYNAVADTLEIINDTIRQSGSEPPKDTIILEQLKISLPL 480  
 Qy 420 ERMGITKTFQPODSREYKVEYNAVADTLEIINDTIRQSGSEPPKDTIILEQLKISLPL 479  
 Db 481 YSILSALTILGIMTASAFLEFNIRNOKLIKMSPPYNNLILGMLSYASTIFLFGIDG 540  
 Qy 480 YSILSALTILGIMTASAFLEFNIRNOKLIKMSPPYNNLILGMLSYASTIFLFGIDG 539  
 Db 541 GSPSEKTEFTLCTVTRTWILTVGYTTAFSGAMFAKTWRVHAIFKNVKKKKIINDOKLLVTV 600  
 Qy 540 GSPSEKTEFTLCTVTRTWILTVGYTTAFSGAMFAKTWRVHAIFKNVKKKKIINDOKLLVTV 599  
 Db 601 VGMILLIDCLICQWAVDPLRTRVERYSMEPPDPAGRDISIRPLEGENTHMTWLTGLTV 660  
 Qy 600 VGMILLIDCLICQWAVDPLRTRVERYSMEPPDPAGRDISIRPLEGENTHMTWLTGLTV 659  
 Db 661 YAYKGLMLFEGCFIAMETRVNSIPALNDSKYIGMSYVNGIMCIIGAASFILRDOPNVOF 720  
 Qy 660 YAYKGLMLFEGCFIAMETRVNSIPALNDSKYIGMSYVNGIMCIIGAASFILRDOPNVOF 719  
 Db 721 CIYALVLIIFCSTITLCLVFPRLITLKNPDAONRFOFTONOKKEDSKTSTVTSYN 780  
 Qy 720 CIYALVLIIFCSTITLCLVFPRLITLKNPDAONRFOFTONOKKEDSKTSTVTSYN 779  
 Db 781 QASTSRLEGQSNHRLRKITELDKLEBYTMOLODPRETTYIKONHGOELNDLSIG 840

OY 780 NQASRRLGLOSENHRRLMKITELDKLEBYTQLODPREKTYIKONHYOELNDISL 839

Db 841 GNFTSTDSGKALIKNHLNDONPOLOMNTTEPSRTCKPDIEDINSPEHIOFRLSLQPLILH 900

OY 840 GNFTSTDSGKALIKNHLNDONPOLOMNTTEPSRTCKPDIEDINSPEHIOFRLSLQPLILH 899

Db 901 HATLPSTIGVDASVPCVSPASPRHRHPPSPRVAVSGI 941

OY 900 HATLPSTIGVDASVPCVSPASPRHRHPPSPRVAVSGI 940

RESULT 3  
ID OY133 PRELIMINARY: PRT: 1221 AA.

AC OY133: 01-NOV-1999 (TREMREL. 12, Created)  
DT 01-NOV-1999 (TREMREL. 12, Last sequence update)  
DT 01-NOV-1999 (TREMREL. 12, Last annotation update)  
DE BCDNA.GH07312.  
GN BCDNA.GH07312.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephyroidea; Drosophilidae; Drosophila.

RP SEQUENCE FROM N.A.  
RA RUBIN G.M., WAN K.H., HARVEY D., LEWIS S.E., BROKSTEIN P., TSANG G.,  
RA AGARANT A., ARCAINA T.J., BAYTER E., BLAZED R.G., BUTENHOFF C.,  
RA CHAMPE M., CHAVEZ C., CHEW M., DOYLE C.M., FARAN D.E., FRISKE E.,  
RA GALLE R., GEORGE R.A., HARRIS N.E., HOSKINS R.A., EVANS-HOLM M.,  
RA HOUTSON K.A., HUMASRI S.R., KIM E., LI P., MOSHEEPI M., PACER J.M.,  
RA PARK S., SEQUEIRA A., SETHI H., SNIR E., SVIRSKAS R.R., WEINBURG T.,  
RA CELINKER S.E.;  
RT "Full length Drosophila melanogaster cDNA sequence."  
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF145639; RAND38614.1;  
SQ SEQUENCE 1221 AA: 138124 MW: CE3B7865 CRC32;

Query Match 32.3%; Score 2234; DB 5; Length 1221;  
Best Local Similarity 41.5%; Pred. No. 0.00e+00;  
Matches 323; Conservative 195; Mismatches 239; Indels 21; Gaps 17;

Db 18 WSTACGRTARSD-VYIAGFPYGGDVENSYTGRCVMSVYKALGHNHGKILANTRLH 76  
OY 41 WTRKAPRPPSPPLSLIMGLMPLTKEVAKSGRGVLPVAVELAEQIRNS-LIRPFLD 99  
Db 77 MMTNDTQCNAAVGVKSFPMHSGPNKVMFGAAGCTHTDPIAKSKHMLTQLSYDTH 136  
OY 100 LRLDTEDCDNAKGLKAFYDAIKYGNHLMVFGVCPSTSIASLQGMNLVOLFSAAT 159  
Db 137 PMFT-KDAPNFRVYSENAPRLLAKFENMTRVGTGYQNEPRYSLPNHNVDLD 195  
OY 160 PVLADKKKKYFFRYPSDANVAPALIKLHFRMRRTGLDQVRFSEVRNDLGVLY 219  
Db 196 AMEEVETQSFVNDVAESLKLRENDVAILIGNENEPKAKACEAKLDMYRAVQL 255  
OY 220 GEDIEIDTSEFSDNPTSVKRLKGDVRIILGFDQNNAAVSCCAEESMFSKQWMI 279  
Db 256 IMATYSTDWN-V-TQ-DSE-CSEIEIATLEGALIVLPLTSGDITVAGITADELY 311  
OY 280 IPGVYEPAMWEGYHVEANSSRLRSLLAAMEGYIGVDFEPLSSQKITISGKTPQYER 339  
Db 312 EYDLR-CTEYSRFGTYDGTMA-A-AL-V-AIOYV-AKRPDLTHHDYVAKMSEVFL 365  
OY 340 EYNSKSGVGPGRKGYADGIVAKTLQRAMETLHASSRQRIQDFNYDHTLGLKIL 399  
Db 366 EALNTEFEVGTGVPYENNERKANILINQFOLGOMEKIGEYHSOKSHLDSLCKPVKW 425  
OY 400 NAMEINTEFFGVYFRNGERMGITIKTOFODSREVKGEYNAVADLEI-INDIRFO 458  
Db 426 GKTPKXRTILYIHSOVNPTIYASASVGIATVFLAFNFKYNOYIKMSPHL 485  
OY 459 GSPEPKKTIITLRLKRIISLPLISLALTILGMASAFLEFNNKNNQNLIMSSPYM 518

Db 486 NNIIIVGCMNTYLSIFIGLDTTSSVAAPYICTARANTIMAGFSLSGAMFSTKRVH 545

OY 519 NNIIIGGLSLASIFLGLDGSFVSERTECTCTVWTLIVGYTAGAFATMAYH 578

Db 546 SIFDTLKKRKIKYQOLFVAVGLAIDAIITWQIADPEFRETQDEPLHNNID-D 604

OY 579 AIFKNVKKMKIKIKQKRLVIVGMLLIDLCILICWAVDPL-RFTVERYSNEPPAGHD 637

Db 605 VLVIPNEVCOSEHNTIVSTIYAKGLLVFGAFAMERHNSISALDSKHIFSVYN 664

OY 638 ISTRPLEHCENTHMTWLGIVAYKGLMFGCFAMETRNVSIPALDSKXIGASVYN 697

Db 665 VFTICAGAAISLVSDRKLDFVLLSFIIFFCTATCLVFPKLVLEKRPQGV-DK 723

OY 698 VGIICIGAAVSFLRPDPNVQFCIVALVIFCSTILCVFVPKILITRTNPDATONR 757

Db 724 RVNATLRPKSKGRDSSVCELEQ---RLDYNNTCRRKALMKENEDLALRL 777

OY 758 RFOFTONKEDSKTISTVSYNASTSRLEGLOSENHRRLMKITELDKLEBYTQLO 815

RESULT 4  
ID OY6022 PRELIMINARY: PRT: 844 AA.

AC OY6022: 01-MAY-1999 (TREMREL. 10, Created)  
DT 01-MAY-1999 (TREMREL. 10, Last sequence update)  
DT 01-MAY-1999 (TREMREL. 10, Last annotation update)  
DE GABAB RECEPTOR, SUBUNIT 1B, PRECURSOR.  
GN GABAB-R1 OR GABA-B R1B OR GABBR1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.

RP SEQUENCE FROM N.A.  
RA WHITE J.H., WISE A., MAIN M.J., GREEN A., FRASER N.J., DISNEY G.H.,  
RA BARNES A.A., EMSON P., FOORD S.M., MARSHALL F.H.,  
RT "Heterodimerisation is required to form a functional GABAB receptor."  
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.  
RA TISSUE-CEREBELLUM:  
RC MEDLINE: 99061981.  
RA KAUPEMAN K., SCHUDER V., MOSBACHER J., BISCHOFF S., BITTGER H.,  
RA HEID J., FROESTL W., LEONHARD S., PRAPF T., KARSGHIN A., BETTER B.,  
RT "Human gamma aminobutyric acid type B receptors are differentially  
expressed and regulate inwardly rectifying K<sup>+</sup> channels."  
RL Proc. Natl. Acad. Sci. U.S.A. 95:14991-14996(1998).

RP SEQUENCE FROM N.A.  
RA YOUNGER R.;  
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ012186; CAA09940.1;  
DR EMBL: AJ225029; CAA12360.1;  
DR EMBL: AL031983; CAA21454.1;  
KW Signal; Receptor.  
FT SIGNAL 1 29 POTENTIAL.  
FT CHAIN 30 844 GABAB RECEPTOR, SUBUNIT 1B.  
SQ SEQUENCE 844 AA: 95148 MW: C7342B77 CRC32;

Query Match 24.4%; Score 1684; DB 4; Length 844;  
Best Local Similarity 35.3%; Pred. No. 0.00e+00;  
Matches 254; Conservative 191; Mismatches 255; Indels 19; Gaps 17;

Db 40 SRVDPHPSERRAVYIGALFPMYS-G-GWPG-GQACQPAVEMALSDVNSRDILPYELKL 96

OY 42 TRGAPRPSPSPSLIMGLMPLTKEVAKSGRGVLPVAVELAEQIRNE-SLRPFLDL 100

Db 97 IHDSCDPCQATKYLYELLYNDPIKILIMP-G-CSSVSTLVAEARMNLIIVLSSSSP 155

OY 101 RLVTEDCDNAKGLKAFYDAIKYGNHLMVFGVCPSTSIASLQGMNLVOLFSAATP 160

Db 156 ALSNRQRFPPFFFTHPSSALNHPTRVKKLEKMGKKINTIQGTTEVFTSLDLEVRVE 215

QY	161	VLADKRYKYYFFRTYSPDPAVPMKLNKQDARITVGLFYEAKAKYPCVYKRLFGKKYWF	220
Db	216	AGLEIFRPSFSDPAVPMKLNKQDARITVGLFYEAKAKYPCVYKRLFGKKYWF	275
QY	221	EDLEISDTSFSBNDPCTSKYKLGNDRIHILGGDDMAAKAFCAFESMGSYQWTI	280
Db	276	IGWYADNWF-KIY-DP-SINCTVDENTEAEGHITTEIYELMANPANTSISNNTSOEFYER	332
QY	281	PGMYEDPAMEOVHVEANSRCLRSRLAAMGVIQVDFEPLSKQIKTISGKTPOOY-ER	339
Db	333	LTRLRHPEEYGFGEAPALADATMALALANTSGS--GGSGYALDEDFYNNQITTD	390
QY	340	EYNS-KRSGVPSKPH-G-YADGIVWIAKTQLQAMETHLASSRHQRIDDFNYDHTLGK	396
Db	391	QIYRANSSSFBYGSYGHVYFSDASSGRANMILDELQGSYKTKIGYDSTKXDSLH-SKTD	449
QY	397	TIIMANNEFEGVGOYVF-RNGERMGITKEFQFQDSREVKXGEENAAADLEIINTI	455
Db	450	KWIGSPPADQTLVTKITERFLSOKIFETSVLSSLSIGLIVLAWCLSPNIYSHVRYIONSQ	509
QY	456	RFGSGEPMDKTIIEQLKISLIPYSLTSLATILGIMASAFLEFNINRQKLIKMS	515
Db	510	PNNNLTAVGCSIALAAVFPGLDGYHGNRQPFVGOARLWTLGSGESLGYSGSEFTIW	569
QY	516	PYNNNLTILGMLSTASIFILGLOSQVSEKTEFTLCYKWTLYLWYGTITAGAAEATW	575
Db	570	WHTVTFTKKEKKEMKRLTEPKLTAAYGLVGMVLTIAIMQYDPLHRTIEFAKEEP	629
QY	576	RVAHIF-KNVKKR-KKIIKQKLLVYIGMLLIDLCILCOWAADPLRRTYERSMSPD	632
Db	630	KEDIVSILPOLHSGSSRKMTWLGIFGYKGLLLGLIFLAEYKSTEKINDHRAVY	689
QY	633	PAGRDISIRPLEHCENHTMTIWLGIYAYXGLMLFGCLAEETRNVSIPALNDSKYIG	692
Db	690	MAIYNAVLCITAPMTLISQODAAFAFSLAIYSSVITLVYFVKMRLLTRGE	748
QY	693	MSYVYNGIMCIIGAAVSPLTRQNPVQCIYALVITICSTITLCIVFYKLTLLTINTD	751
RESULT 5			
ID	Q92308	PRELIMINARY;	PRT; 812 AA.
AC	Q92308;		
DT	01-MAY-1999 (Tremblrel. 10, Created)		
DT	01-MAY-1999 (Tremblrel. 10, Last sequence update)		
DE	01-MAY-1999 (Tremblrel. 10, Last annotation update)		
DE	GABAR RECEPTOR 1D.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE-CEREBELLUM;		
RA	MEDLINE; 99092370.		
RA	ISOMOTO S., KAIIBARA M., SAKURAI-YAMASHITA Y., NAGAYAMA Y., UEZONO Y.,		
RA	YANO K., TANIYAMA K.;		
RT	"Cloning and tissue distribution of novel splice variants of the rat		
RT	GABAR receptor.";		
RL	Biochem. Biophys. Res. Commun. 253:10-15(1998).		
DR	EMBL: AB016161; BAA34709.1. -		
KW	RECEPTOR		
SO	SEQUENCE	812 AA; 90920 MW; 566B90A CRC32;	
Query Match			
	24.3%;	Score 1680; DB 11; Length 812;	
	Best Local Similarity 35.1%;	Pred. No. 0.00e+00;	
	Matches 262; Conservative 192; Mismatches 269; Indels 23; Gaps 21.		
Db	13	PPLPLVMAAGVAVPVAHSP-HLPRPVRVPPSPSERAAVYIGAL-PPMSGGWPQ-GQ 69	
QY	19	PARULPILILSL-LMLAGAMGWIRGAP-R-PSSPPLST-MGLMPLTKRYAAGSICR 74	
Db	70	ACQAVMALEADVNSKRDLIPYEKLTHDSCDDPCQCATKYITELLVNDPIKTIIMPQ- 128	

QY	75	GVLPAAVELAQEIRNE-SLAPFLYDLRLVDFECBDNAKGLKAFYDAIKYGGPHLMFVGV	133
Db	129	CSSVSTLVAAARMNLVLYSYGSSSPALSNRRPPTFPRTPSATLHNPRTVLFKMG	168
OY	134	GPSTVILNESIQGNQVLQSPFAATVTLADKKRTVFRTPVSDNANVATLTKLHFR	193
Db	189	WKRIATIQGTTEVTSTUDDLEEVNKAEGLITFRQSFSDPAVPEVKNLKRQDARIYGL	248
OY	194	WRERGTLTDOVORFEVEVKNDDLTGVLGEDEIDTSDTESFNDCTSYKKLKNDRVILLGO	253
Db	249	FYTEERKRFCEVYKERLFGEKKYVWFLICGVYAAVNW-KTY-PP-SINCTVEAMTAEVGH	305
OY	254	FDQNMARVFCFCAEDFESVSGKQMIIPGWYEPAMWQYHVAENSRCGLRSLLAABGY	313
Db	306	ITTEIYMLNPATBRSISMVSOFEVEKLTRLKRHEDEFGQOEARPLAYDAITMALALN	365
OY	314	IGVDFEPLSSKOIKITISKTPOQT-EKEVNS-KRSGVPSKTH-G-YAIDGIMVIAKTLO	369
Db	366	KTSGG--GGRSGVRLDEDVNNQOTITDOIYRANSSSFEVSGHYVFDASGRMAWTLIE	423
OY	370	RAEETHASSRQRIODPNPYNDHTLGKILINMANENFEGVIGQVVF-RNGBRGITIKFT	428
Db	424	QLOGGKYKIGYSDTRKDLMS-SKTPKRWGSGPPDOQLVTKTFRPFISOKLFTSVLS	482
OY	429	QPDSEKVEKGVENAVATLTELINDTIRFGSGEPDPDKTILIEOLKRLSLPSLTSLMT	488
Db	483	SLGIVAVVCLSPNINSHVARYIONSONPUNNTFVCGSLAALAAVPLGLDGIHGRSQF	542
OY	489	ILDMIASAFLEFNKNNQGLIKMSSPYNNMLILIGMISYASLPLDGLDSFVSEKTF	548
Db	543	PFVCOARWLILGISTLGYSGMFTKIMVHTVETFKKERKRLTEPWLKYATVGLLVG	602
OY	549	ETICTFRTMLTVGGTTFAGMAFKTRVHAIF-KNVKMK-KKIIKQKRLVIYGGMLL	605
Db	603	MDVLTALMOIYDPLHPTIEFFAKEBEKEDIVSIIIPOLHSCSKMNTWGIIFYGKGL	662
OY	606	IDCILICLMOADPLRKRYEKESEPPADRODISIRPLEHCEGHHMTIWLGIYAAKGL	665
Db	663	LILIGFLAVETPKSVSTERKINDHRAVGMALYNAVLCITAPYTMILSSQDAAFAFRSL	722
OY	666	LMFGEFLMERNVNISALNDSKRTICKMSYVNGIMCITGAAVSFLTRDPQVOCFVAL	725
Db	723	AIYESSITLVLPVKMRRLTRIGE 748	
OY	726	VIIFCSTITLCLVPVKILITRTMPD 751	
RESULT	6		
ID	03WV15	PRELIMINARY: PRT; 833 AA.	
AC	03WV15		
DT	01-NOV-1999 (TREMBLrel. 12, Created)		
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)		
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)		
DE	573K1.1.4 (GAMMA-AMINO BUTYRIC ACID (GABA) B RECEPTOR, 1D).		
EN	573K1.1.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
NC	[1]		
RP	SEQUENCE FROM N.A.		
RA	YOUNGER R.		
RL	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AL078630; CAB44993.1; -.		
KM	Receptor.		
SO	SEQUENCE 833 AA; 93167 MW; 0C07A359 CRC32;		
Db	Query Match	24.3%; Score 1681; DB 11; Length 833;	
OY	Best Local Similarity	35.1%; Pred. No. 0.0e+00;	
	Matches	262; Conservative 192; Mismatches 269; Indels 23; Gaps 21.	
Db	13 PRLPILVMAAGVAPVWASHSP-HLPRRHPVPPHPSERRAYITGL-FPMSCGPG-GQ 69		
OY	19 PARLLPILVLSL-LWLPAGMGWTRGAP-PP-PSSPLSLT-MGLMPLTEKVAAGSTGR 74		

RESULT	7	PRELIMINARY:	PRT:	844 AA.
ID	09WV17			
AC	09WV17;			
DT	01-NOV-1999 (TREMBLrel. 12, Created)			
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)			
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)			
DE	573K1.1.2 (GAMMA-AMINOBUTYRIC ACID (GABA) B RECEPTOR, 1B).			
GN	573K1.1.			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Mammalia;			
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
	[1]			
RN	SEQUENCE FROM N.A.			
RP				
RA	YOUNGER R.;			
RL	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AL078630; CAB44991.1; -			
	Receptor.			
SO	SEQUENCE	844 AA;	95022 MW;	96F2ED2A CRC32;
Query Match		24.3%;	Score 1681;	DB 11;
Best Local Similarity		35.1%;	Pred. No. 0.00e+00;	
Matches	262;	Conservative	192;	Mismatches 269;
				Indels 23;
				Gaps 21

RESULT	8	PRELIMINARY;	PRT;	844 AA.
ID	008621			
AC	008621;			
DT	01-JUL-1997	(TIREMBLrel. 04, Created)		
DT	01-JUL-1997	(TIREMBLrel. 04, Last sequence update)		
DT	01-MAY-1999	(TIREMBLrel. 10, Last annotation update)		
DE	GABA-B1B RECEPTOR			
GN	GABA-B1B OR GABAB1.			
OS	Rattus norvegicus (Rat.).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
RM	{1}			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-T1F (RAI F1(SPF)); TISSUE=CORTEx, AND CEREBELLUM;			
FX	MEDLINE. 97222131.			
RA	KAMPAWANN K., HEGSEL C., HEID J., FLOR P. J., BISCHOF S., MICHEL S. J. . .			
RA	ROHMERTER G., ANGST R., BITTIGER H., FROESTL W., BETTLER B. ;			
RT	"Expression cloning of GABA(B) receptors uncovers similarity to			
RT	metabotropic glutamate receptors.";			
RL	Nature 386:239-246(1997).			

[12]  
SEQUENCE FROM N.A.

RC STRAIN-WISTR;  
RA PRAFF T., MULLISCHER B., KUPPMANN K., BETTLER B., KARSCHIN K.;  
RT "Alternative splicing generates a novel isoform of the rat  
metabotropic GABAB receptor";  
RL Eur. J. Neurosci. 0:0-0(1999).  
DR EMBL; Y10370; CAA71399.1; -  
DR EMBL; AF110797; AAD19657.1; -  
DR EMBL; AF110797; AAD19657.1; JOINED.  
DR PFAM; PF00003; 7tm.3; 1.  
DR PFAM; PF01094; ANF\_receptor; 1.  
KW Receptor.

SEQUENCE 844 AA; 95037 MW; 6611680 CRC32;

Query Match 24.3%; Score 1680; DB 11; Length 844;  
Best Local Similarity 35.1%; Pred. No. 0.00e+00;  
Matches 262; Conservative 192; Mismatches 269; Indels 23; Gaps 21;

Db 13 PLPLLYMAVAVPVAWASHP-HLPRPRVPRPSPSSERRAVYIGAL-FPMGSGMPG-GQ 69  
Qy 19 PARLLPLLLSL-LWLAPGAWGTGAPR-PP-SSPLSLI-MGLMPLTKKVAKSGISGR 74  
Db 70 ACQAVMALEEDVNSRDIDPEYELKLIHDSKODPGATKYELLYNDPIKILMPG- 128  
Qy 75 GVLPAVELAEQIRNE-SLRPFELDLRYTECDNAGLKAFTDAIKYGNHLMFEGV 133  
Db 129 CSSVSTLVAFAAMMNLIVLSTGSSPALSNSRQREFTEFTRPSATLHNPVRLKFEKW 188  
Qy 134 CPVSTSIASLQGMNLVOLSFPAATTPVLADKKKPYFFRTVPSPDNVNAFALIKLHPR 193  
Db 189 WKATATQCTTEVFTSLDLEERYKAGIEITRFOSFSDPAPVAVNLRQDARIYVL 248  
Qy 194 WRVGTLTQOVQFSEVRNDLGVLYGEDIEISDIESNDPCISVKKLKGNDVRIILGO 253  
Db 249 FYEFAKRVCEYKKEKELGKYVFLGWADNMF-KTY-DP-SINCTVDEMTTEVEH 305  
Qy 254 FDQMAAKAVCCAFESMFGSKYQWIIPOWEPYPAWDEYHVAANSCLRLSLANMEY 313  
Db 306 ITTEIYVMPANTRRSISNMTSOEVEKLTRLKRHEEFTGSGFQAPLAYDAIMALALN 365  
Qy 314 IGVFPEPLSKQIKTISGKTPQY-EREVNS-KRSGVPSKTH-G-YAYDGIWVIATKO 369  
Db 366 KTSGG--GGRSGVRLDEPNYNNQITDOIYRAMNSSFEVSGHVFDASGSHAMTLIE 423  
Qy 370 RAMETLHASSRHQRIODENYTDHIGKILNMANNEFVGTVGQVVF-RNGERMGTIKET 428  
Db 424 OLOGGSKTKIGYDSTKDDLSW-SKTDKWIIGSPADOTLVIKTRFLSKLISVSVLS 482  
Qy 429 QFQDSREYKVEYNAVADTEIINDTIRQSGSEPKDKTIILEDKRTISLPLISILALT 488  
Db 483 SLGIIVAVCLSPNIYNSHVRIONSOPNLNLTAVGCSIALAAVFLGLDGYHIGRSQF 542  
Qy 489 ILGIMASAFLEFNKRNOKLTKMSSPYNNLILGMLSYAIFLFGDSGFSVEKTF 548  
Db 543 PFVQCARMLLGLGSLGSGSMFTKIMWVHTFTKKEKEMRRTLEPMVLVYFVGLG 602  
Qy 549 ETLCTVMTLIVGYTTATGAMAKTRWHAIF-KNVKMK-KKIIIDQGLLVIVGMLL 605  
Db 603 MDVLTALINQIADPLHRTIETFAKEPKEDIVSLIPOLEGSSKRNMTLGIFFYKGL 662  
Qy 606 IDLICILICQWAVDPLRRTVERYSMEPDAGRDISIRPLEHCENTHTIWLGIYAVKYL 665  
Db 663 LLLGLFLAETKSVSTEKINDHRAVGAIVYNAVCLITAPVTMILSSOODAFAFAF 722  
Qy 666 LMLFGCLAWETRNVSIPALNDSKYIGMSVYVNGICIIIGAASFILTRDQPNVQCIYAL 725  
Db 723 AIVSSYITLVVLEVPKMRLLTRGE 748  
Qy 726 VIFCSITITCLVVPKRLITLRINPD 751

RESULT 9

ID 095975 PRELIMINARY; PRT: 899 AA.

AC 095975.  
DT 01-MAY-1999 (Tremblrel. 10, Created)  
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)  
DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)  
DE GABAB RECEPTOR, SUBUNIT 1C, PRECURSOR.  
GN GABAB-R1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
[1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=CEREBELLUM;  
RA WHITE, J.H., WISE A., MAIN M.J., GREEN A., FRASER N.J., DISNEY G.H.,  
RA BARNES A.A., EMSON P., FOORD S.M., KARSCHIN K., KARSCHIN F.H.,  
RT Heterodimerisation is required to form a functional GABAB receptor.;  
RL Submitted (Oct-1998) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AJ012187; CAA09941.1; -  
KW Signal; Receptor.  
FT SIGNAL 1 17 POTENTIAL.  
FT CHAIN 18 899 GABAB RECEPTOR, SUBUNIT 1C.  
SQ SEQUENCE 899 AA; 101551 MW; 04619FDC CRC32;

Query Match 24.3%; Score 1676; DB 4; Length 899;  
Best Local Similarity 36.0%; Pred. No. 0.00e+00;  
Matches 248; Conservative 179; Mismatches 245; Indels 16; Gaps 14;

Db 123 GQACQPAVEMALEDVNSRDIDPEYELKLIHDSKODPGATKYELLYNDPIKILMP 182  
Qy 73 GRVLPVAVELAIQDIRNE-SLRPFELDLRYTECDNAGLKAFTDAIKYGNHLMFVG 131  
Db 183 G-CSSVSTLVAFAAMMNLIVLSTGSSPALSNSRQREFTEFTRPSATLHNPVRLKFEK 241  
Qy 132 GVCPSVSIASLQGMNLVOLSFPAATTPVLADKKKPYFFRTVPSPDNVNAFALIKLH 191  
Db 242 WKKATATQCTTEVFTSLDLEERYKAGIEITRFOSFSDPAPVAVNLRQDARIYVL 301  
Qy 192 FRKRVGTLTQOVQFSEVRNDLGVLYGEDIEISDIESNDPCISVKKLKGNDVRIIL 251  
Db 302 GLYEYERAKRVCEYKKEKELGKYVFLGWADNMF-KTY-DP-SINCTVDEMTTEVEH 358  
Qy 252 GQFDONMAKAVCCAFESMFGSKYQWIIPOWEPYPAWDEYHVAANSCLRLSLANMEY 311  
Db 359 GHITTEIYVMPANTRRSISNMTSOEVEKLTRLKRHEEFTGSGFQAPLAYDAIMALALA 418  
Qy 312 GYIGVDFPEPLSKQIKTISGKTPQY-EREVNS-KRSGVPSKTH-G-YAYDGIWVIATK 367  
Db 419 LNKTSGG--GGRSGVRLDEPNYNNQITDOIYRAMNSSFEVSGHVFDASGSHAMTL 476  
Qy 368 LQRAMETLHASSRHQRIODENYTDHIGKILNMANNEFVGTVGQVVF-RNGERMGTIK 426  
Db 477 IEOLGGSKTKIGYDSTKDDLSW-SKTDKWIIGSPADOTLVIKTRFLSKLISVSVS 535  
Qy 427 FTOFQDSREYKVEYNAVADTEIINDTIRQSGSEPKDKTIILEDKRTISLPLISILALT 486  
Db 536 LSLGLIYAVVCLSPNIYNSHVRIONSOPNLNLTAVGCSIALAAVFLGLDGYHIGRN 595  
Qy 487 LILGIMASAFLEFNKRNOKLTKMSSPYNNLILGMLSYAIFLFGDSGFSVSK 546  
Db 596 OPPEYQCARMLLGLGSLGSGSMFTKIMWVHTFTKKEKEMRRTLEPMVLVYFVGLG 655  
Qy 547 TFEELCTVMTLIVGYTTATGAMAKTRWHAIF-KNVKMK-KKIIIDQGLLVIVGMLL 603  
Db 655 VQMDVLTALINQIADPLHRTIETFAKEPKEDIVSLIPOLEGSSKRNMTLGIFFYKGL 715  
Qy 604 LILDCILICQWAVDPLRRTVERYSMEPDAGRDISIRPLEHCENTHTIWLGIYAVK 663  
Db 716 GLLLGLFLAETKSVSTEKINDHRAVGAIVYNAVCLITAPVTMILSSOODAFAFAF 775  
Qy 664 GLMLFGCLAWETRNVSIPALNDSKYIGMSVYVNGICIIIGAASFILTRDQPNVQCIY 723  
Db 776 SLAIVSSYITLVVLEVPKMRLLTRGE 803

Qy 724 ALVITFCSTITLCLVFPKLTITRTND 751

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RESULT 10
ID 095375 PRELIMINARY; PRT: 961 AA.
AC 095375;
DT 01-MAY-1999 (Tremblrel, 10, Created)
DT 01-MAY-1999 (Tremblrel, 10, Last sequence update)
DT 01-NOV-1999 (Tremblrel, 12, Last annotation update)
DE GABA-BLA RECEPTOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA STRIPP U., RAMING K.;
RT "Human mRNA for GABA-Bla receptor."
RT Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF099148; AAC98508.1;
DR HSSP; P10998; IYVC.
KW Receptor.
SQ SEQUENCE 961 AA; 108336 MW; 14545CBE CRC32;

Query Match 24.3%; Score 1676; DB 4; Length 961;
Best Local Similarity 36.0%; Pred. No. 0.00e+00;
Matches 248; Conservative 179; Mismatches 245; Indels 16; Gaps 14;

Db 185 GACACPAVMALEEDVNSRRDLPYELKLHDSKCDPGATKYLYELLNPKITLMP 244
Qy 73 GRCVLPVAVLAEIOIRNE-SLRPFYDLRLYTECDNAGLAFYDAIKYGNHLMVFG 131
Db 245 G-CSSVSTLVAABARMNLIVSYGSSPALSNRPFRTFPATLHNPTRVLFEX 303
Qy 132 GVCPSVSTLVAASLOGMNLVOLFATIPVLAADKKKPYFFRTVPSDMANPRLILKLN 191
Db 304 WKKKATATQOQTEVFTSLDLERYKAEIETTFROSPDPAPVYKLRKQDARIIV 363
Qy 192 FRRRRGITLQVORSEVRNDLTGLVGEDIEISDESSNDPCISVKKLKGNDVRILL 251
Db 364 GLFYEETARKVCEVYKKEFLFGKKYVFLIGVADNMF-KIY-DP-SINCTVDEMTAVE 420
Qy 252 GQPDQMAKAVVCCAFEEESMGSKYQWIIIPGWPAMWQVHYEANSRCLRSLLAAAE 311
Db 421 GHTTTEIVLNPANTRISNMTSOFVFKLTKRKHPDEETGQEPAPLAYDAITALA 480
Qy 312 GYIGVDFEPLSSKQKITISGKTPQY-BREYNS-KRSGVPSKFH-G-YAYDGIWIAKT 367
Db 481 LKRTSGG--GGRSGVRLDEDFNNQITDQIYRAMNSSSEEGVSGHYVDPASGRAMTL 538
Qy 368 LQAMETLHASSRHQRIODFNTHLTKILNMANETNEFGVGVYF-RNGERMGTIK 426
Db 539 IELOGSVKKIKGYSTKDDLSW-SKTDKMTGSGPRADQIYKTRFISQKLFSTISGV 597
Qy 427 FTQFQREYKKEGNAVADTLEITINDIIRGSGEPPOKTIIEQIRKISLPLYSILSK 486
Db 598 LSSSLGIVAVCLSFNINSHVYIIONSOPLNLTAVGCSLAAVPLGLDGYHIGN 657
Qy 487 LITLIGIMASALFENIKRNOKLTKMSSPYNNLIIIGWLSYASIFLLGLDGSFVSEK 546
Db 658 OPFVCOARWMLGLGFSLGYSMTKIMWVHTVFTKKEEKERKLTPEMKLYATVGLL 717
Qy 547 TFEFLCIVRWILTYGTTAFGAMFAKTYRHAIF-KNVKMK-KKTIKQOKLIVYGGH 603
Db 718 VGMVDVLTALVQIDPLARTIETFAKEEPKEDIVSLIPOLEHSSKRMNTWLGIFYGK 777
Qy 604 LILDLCLLQMAVDLRLRTVERYSWEDPAGRODISIRLLEHEDNHTMIWIGIAYYAK 663
Db 778 GLLLILGIFLAEETKSVTEKINDBRAGMAIYNAVAVCLITAPVTMILSODDAAFAFA 837
Qy 664 GLMLRECFCLAMETRNVSIPALNDSKYSIMSYNGIMCIIGAAVSLTLDQDPVQFCIV 723
Db 838 SLAIVSSITTLVVLFPKMRLLTRGE 865

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Qy 724 ALVITFCSTITLCLVFPKLTITRTND 751

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RESULT 11
ID 095468 PRELIMINARY; PRT: 930 AA.
AC 095468;
DT 01-MAY-1999 (Tremblrel, 10, Created)
DT 01-MAY-1999 (Tremblrel, 10, Last sequence update)
DT 01-NOV-1999 (Tremblrel, 12, Last annotation update)
DE GABABRI PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA PETERS H.C., KAEMER G., VOIZ A., KAUPMANN K., ZIEGLER A., BETTLER B.,
RA EPPLEN J.T., SANDER T., RIESS O.;
RT Mapping, genomic structure and polymorphisms of the human gababrl
RT receptor gene: evaluation of its involvement in idiopathic generalized
RT epilepsy.
RL Neurogenetics 2:47-54(1998).
DR EMBL; AJ010170; CAA09031.1; JOINED.
DR EMBL; AJ010171; CAA09031.1; JOINED.
DR EMBL; AJ010172; CAA09031.1; JOINED.
DR EMBL; AJ010173; CAA09031.1; JOINED.
DR EMBL; AJ010174; CAA09031.1; JOINED.
DR EMBL; AJ010175; CAA09031.1; JOINED.
DR EMBL; AJ010176; CAA09031.1; JOINED.
DR EMBL; AJ010177; CAA09031.1; JOINED.
DR EMBL; AJ010178; CAA09031.1; JOINED.
DR EMBL; AJ010180; CAA09031.1; JOINED.
DR EMBL; AJ010181; CAA09031.1; JOINED.
DR EMBL; AJ010182; CAA09031.1; JOINED.
DR EMBL; AJ010183; CAA09031.1; JOINED.
DR EMBL; AJ010184; CAA09031.1; JOINED.
DR EMBL; AJ010185; CAA09031.1; JOINED.
DR EMBL; AJ010186; CAA09031.1; JOINED.
DR EMBL; AJ010187; CAA09031.1; JOINED.
DR EMBL; AJ010188; CAA09031.1; JOINED.
DR EMBL; AJ010189; CAA09031.1; JOINED.
DR EMBL; AJ010190; CAA09031.1; JOINED.
DR EMBL; AJ010191; CAA09031.1; JOINED.
DR HSSP; P10998; IYVC.
SQ SEQUENCE 930 AA; 104564 MW; B825E4F7 CRC32;

Query Match 24.2%; Score 1671; DB 4; Length 930;
Best Local Similarity 36.0%; Pred. No. 0.00e+00;
Matches 248; Conservative 180; Mismatches 243; Indels 17; Gaps 15;

Db 185 GACACPAVMALEEDVNSRRDLPYELKLHDSKCDPGATKYLYELLNPKITLMP 244
Qy 73 GRCVLPVAVLAEIOIRNE-SLRPFYDLRLYTECDNAGLAFYDAIKYGNHLMVFG 131
Db 245 G-CSSVSTLVAABARMNLIVSYGSSPALSNRPFRTFPATLHNPTRVLFEX 303
Qy 132 GVCPSVSTLVAASLOGMNLVOLFATIPVLAADKKKPYFFRTVPSDMANPRLILKLN 191
Db 304 WKKKATATQOQTEVFTSLDLERYKAEIETTFROSPDPAPVYKLRKQDARIIV 362
Qy 192 FRRRRGITLQVORSEVRNDLTGLVGEDIEISDESSNDPCISVKKLKGNDVRILL 251
Db 364 GLFYEETARKVCEVYKKEFLFGKKYVFLIGVADNMF-KIY-DP-SINCTVDEMTAVE 419
Qy 252 GQPDQMAKAVVCCAFEEESMGSKYQWIIIPGWPAMWQVHYEANSRCLRSLLAAAE 311
Db 420 GHTTTEIVLNPANTRISNMTSOFVFKLTKRKHPDEETGQEPAPLAYDAITALA 479
Qy 312 GYIGVDFEPLSSKQKITISGKTPQY-BREYNS-KRSGVPSKFH-G-YAYDGIWIAKT 367
Db 480 LKRTSGG--GGRSGVRLDEDFNNQITDQIYRAMNSSSEEGVSGHYVDPASGRAMTL 537

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OY 733 ITLCVFEVKLITLRTNPDATONRRFOFONOKKEDSKISTSVYNQASTSRLEGLOS 792  
Db 61 ENHRLFMKITTELDKDLEEVYTMLODTPPEKTYIKONHYQELNDILNIGNFTSTDGSKAI 120  
OY 793 ENHRLFMKITTELDKDLEEVYTMLODTPPEKTYIKONHYQELNDILNIGNFTSTDGSKAI 852  
Db 121 LKNHLDONPOLQWMTTEPSRTCKDPIEDINSPEHIOURLSLQPLHAYLPSIGVDAS 180  
OY 853 LKNHLDONPOLQWMTTEPSRTCKDPIEDINSPEHIOURLSLQPLHAYLPSIGVDAS 912  
Db 181 CVSPCVSPTASPRHR 195  
OY 913 CVSPCVSPTASPRHR 927

Search completed: Wed Mar 15 22:31:19 2000  
Job time : 1040 secs.



CC	1-1	TISSUE SPECIFICITY: RESTRICTEDLY EXPRESSED IN THE INNER NUCLEAR LAYER OF THE RETINA.
CC	-1	SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC	STRONGEST	TO MGR4.
CC	CC	THIS SWISS-PROT ENTRY IS COPYRIGHT. IT IS PRODUCED THROUGH A COLLABORATION BETWEEN THE SWISS INSTITUTE OF BIOINFORMATICS AND THE EMBL OUTSTATION - THE EUROPEAN BIOINFORMATICS INSTITUTE. THERE ARE NO RESTRICTIONS ON ITS USE BY NON-PROFIT INSTITUTIONS AS LONG AS ITS CONTENT IS IN NO WAY MODIFIED AND THIS STATEMENT IS NOT REMOVED. USAGE BY AND FOR COMMERCIAL ENTITIES REQUIRES A LICENSE AGREEMENT (SEE <a href="http://www.isb-sib.ch/announce/or_send_an_email_to_license@isb-sib.ch">http://www.isb-sib.ch/announce/or_send_an_email_to_license@isb-sib.ch</a> ).
CC	DR	EMBL: D13963; BAA03066.1; -
CC	DR	PIR: A46742; A46742.
CC	DR	GCDDB: GCR_0623; -
CC	DR	PROSITE: PS00979; G_PROTEIN_RECEP_F3_1.1.
CC	DR	PROSITE: PS00980; G_PROTEIN_RECEP_F3_2.1.
CC	DR	PROSITE: PS00981; G_PROTEIN_RECEP_F3_3.1.
CC	DR	PFAM: PF00003; 7tm_3.1.
CC	DR	PFAM: PF01094; ANF_receptor.1.
CC	KW	G-protein coupled receptor; Transmembrane; Glycoprotein; signal; Multigene family; vision.
CC	KW	SIGNAL
CC	FT	CHAIN 1 18
CC	FT	DOMAIN 19 871
CC	FT	TRANSSEM 580 602
CC	FT	DOMAIN 603 616
CC	FT	TRANSSEM 617 637
CC	FT	DOMAIN 638 648
CC	FT	TRANSSEM 649 667
CC	FT	DOMAIN 668 691
CC	FT	TRANSSEM 692 712
CC	FT	DOMAIN 713 742
CC	FT	TRANSSEM 743 764
CC	FT	DOMAIN 765 777
CC	FT	TRANSSEM 778 800
CC	FT	DOMAIN 801 813
CC	FT	TRANSSEM 814 839
CC	FT	DOMAIN 840 871
CC	FT	CARBOHYD 290 290
CC	FT	CARBOHYD 445 445
CC	FT	CARBOHYD 473 473
CC	FT	CARBOHYD 561 561
CC	FT	SEQUENCE 871 AA; 95089 MM; 81A229E4 CRC32;
CC	CC	Query March 3.4%; Score 236; DB 1; Length 871;
CC	CC	Best Local Similarity 22.9%; Pzed. No. 1.10e-19;
CC	CC	Matches 64; Conservative 90; Mismatches 102; Indels 24; Gaps 21;
CC	DB	586 LAVIG-IMATTIMATPEKHANDPIVRAAGRELSYLVLTGIFLITVA-I-TF-L--MYAE 638
CC	QY	487 LTIIGMMAAPLFFFIKRNKOK-LIKSSPYNNKLLIIGMSYASIFLFDLDSFSE 545
CC	DB	639 PC-AIICARRLILGTLTSLATLTKNTIYIFEOGRKSYTPPPTISPSOLVITFG 697
CC	QY	546 KTFELTCTRWILTVGYTTAFGAFAKTAHVAFKXN--MKK-IKDKKLVIYVG 602
CC	DB	698 LLSGVYGVYAMIGADPPHSVID-E-QGRVDEQA-RGVK-CMPSLST-IGCL-GY 751
CC	QY	603 MLILDELTCMOWNDPLARIVERSMPPDAGDISIRPLDHCENTMTITMLGIYAY 662
CC	DB	752 -SLILMWT-C-TYVAIKARGVPTFENKAPDIFGTMYTTCIIMLAFVIFFGTAQSAEKIYI 809
CC	QY	663 KGLIMTFGCILAMETRNNSIP-ALNDSKYIOMSYINVGIIICIGAVSFILTRDPQVQFC 721
CC	DB	810 QTTLLVTSLSASVSLGMLVYPKYVYLFFPEQVQK 849
CC	QY	722 -IYALVI-I-FCSTIILCLVFPKILITIRTNPDAAQNNR 758
CC	RESULT	3
CC	ID	MGR8_RAT
CC	STANDARD:	PRT; 908 AA.

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AC      P70579;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      15-JUL-1998 (Rel. 36, Last annotation update)
DE      METABOTROPIC GLUTAMATE RECEPTOR 8 PRECURSOR.
GN      GRM8 OR MGLUR8.
OS      Rattus norvegicus (Rat.).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC      Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE; 97168760.
RA      SAUGSTAD J.A., KINZIE J.M., SHINOHARA M.M., SEGGERSON T.P.,
RA      WESTBROOK G.L.;
RT      "Cloning and expression of rat metabotropic glutamate receptor 8
RT      reveals a distinct pharmacological profile."
RL      Mol. Pharmacol. 51:119-125(1997).
CC      -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC      IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLYLATE CYCLASE
CC      ACTIVITY.
CC      -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC      -1- TISSUE SPECIFICITY: PROMINENT EXPRESSION IN OLFACTORY BULB,
CC      PONTINE GRAY, LATERAL RETICULAR NUCLEUS OF THE THALAMUS, AND
CC      PIRIFORM CORTEX. LESS ABUNDANT EXPRESSION IN CEREBRAL CORTEX,
CC      HIPPOCAMPUS, CEREBELLUM, AND MAMMARY BODY.
CC      -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; U63288; AAB09537.1; -.
DR      GCRDB; GCR_1411; -.
DR      PROSITE; PS00979; G_PROTEIN_RECPEP_F3_1; 1.
DR      PROSITE; PS00980; G_PROTEIN_RECPEP_F3_2; 1.
DR      PROSITE; PS00981; G_PROTEIN_RECPEP_F3_3; 1.
DR      PFM; PF00003; 7tm_3; 1.
DR      PFM; PF01094; ANF_receptor; 1.
DR      G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW      Multigene family; Olfaction.
FT      SIGNAL 1 33
FT      CHAIN 34 908
FT      DOMAIN 34 583
FT      TRANSMEM 584 608
FT      DOMAIN 609 620
FT      TRANSMEM 621 641
FT      DOMAIN 642 647
FT      TRANSMEM 648 668
FT      DOMAIN 669 695
FT      TRANSMEM 696 716
FT      DOMAIN 717 746
FT      TRANSMEM 747 768
FT      DOMAIN 769 781
FT      TRANSMEM 782 803
FT      DOMAIN 804 818
FT      TRANSMEM 819 843
FT      DOMAIN 844 908
FT      CARBOHYD 95 95
FT      CARBOHYD 298 298
FT      CARBOHYD 452 452
FT      CARBOHYD 480 480
FT      CARBOHYD 565 565
SQ      SEQUENCE 908 AA; 101866 MW; 5043FE81 CRC32;
Query Match 3.4%; Score 236; DB 1; Length 908;
Best Local Similarity 21.9%; Pred. No. 1,10E-19;
Matches 62; Conservative 97; Mismatches 100; Indels 24; Gaps 21;
DB 590 IALGII-ATFEVIVTFVRNDPIYRASGRSLVLLTGIFLCYSITFLM-I-AA--PD 644

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QY      487 ILIIMIMASAFLEFN-ITKNRQKLIKSSPYMNNLLILGMLSYASIFLEGDGSFVSE 545
DB      645 -IT-ICSEFRIFLGLGCFYAAULTKTRNRIHRIFEQGSRYAPRFISASOLVTFPS 701
QY      546 KTFEFLCTVRITWILVGTTFAGAFATWYHAFKRVKAK-K-KIINDQKLVIYVG 602
DB      702 LISVLLGVFWFVVDPPHTIID-YG-EORTLDE-NARGLYK-CDISDSL-ICSL-GY 755
QY      663 KGLIMLFGCFIAMEIRNNSIP-ALNDSKYIGKSYNVGIMCIIIGAASFLTRDPNVOFC 721
DB      814 QTTTLVSWLSASVSLGMLWPKYIIIFHEQNVQKRKSF 856
QY      722 -IVALVT-I-FSTITLCLVFPKILITLRNDATQNRROF 761
RESULT 4
ID      MGR8_HUMAN STANDARD; PRT; 908 AA.
AC      000222; 015493;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      15-DEC-1999 (Rel. 39, Last annotation update)
DE      METABOTROPIC GLUTAMATE RECEPTOR 8 PRECURSOR.
GN      GRM8 OR MGLUR8.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC      Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE; 98141892.
RA      WU S., WRIGHT R.A., ROCKEY P.K., BURGETT S.G., ARNOLD J.S.,
RA      ROSTOPF P.R. JR., JOHNSON B.G., SCHORPP D.D., BELGAJE R.M.;
RT      Group III human metabotropic glutamate receptors 4, 7 and 8:
RT      molecular cloning, functional expression, and comparison of
RT      pharmacological properties in RGT cells."
RL      Brain Res. Mol. Brain Res. 53:88-97(1998).
DR      RP SEQUENCE FROM N.A.
DR      MEDLINE; 97446143.
DR      SCHERER S.W., SODER S., DUVOISIN R.M., HUIZENGA J.J., TSUI L.C.;
RT      "The human metabotropic glutamate receptor 8 (GRM8) gene: a
RT      disproportionately large gene located at 7q31.3-q32.1."
RL      Genomics 44:232-236(1997).
CC      -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC      IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLYLATE CYCLASE
CC      ACTIVITY.
CC      -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC      -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; U92459; AAB51764.1; -.
DR      EMBL; U95025; AAB72040.1; -.
DR      GCRDB; GCR_1889; -.
DR      GCRDB; GCR_2604; -.
DR      MIM; 601116; -.
DR      PROSITE; PS00979; G_PROTEIN_RECPEP_F3_1; 1.
DR      PROSITE; PS00980; G_PROTEIN_RECPEP_F3_2; 1.
DR      PROSITE; PS00981; G_PROTEIN_RECPEP_F3_3; 1.
DR      PFM; PF00003; 7tm_3; 1.
DR      PFM; PF01094; ANF_receptor; 1.
KW      G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW      Multigene family; Olfaction.

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FT SIGNAL 1 33 POTENTIAL.
FT CHAIN 34 908 METABOTROPIC GLUTAMATE RECEPTOR 8.
FT DOMAIN 34 583 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 584 608 I (POTENTIAL).
FT DOMAIN 609 620 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 621 641 II (POTENTIAL).
FT DOMAIN 642 647 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 648 668 III (POTENTIAL).
FT DOMAIN 669 695 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 696 716 IV (POTENTIAL).
FT DOMAIN 717 746 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 747 768 V (POTENTIAL).
FT DOMAIN 769 781 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 782 803 VI (POTENTIAL).
FT DOMAIN 804 818 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 819 843 VII (POTENTIAL).
FT DOMAIN 844 908 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 95 95 POTENTIAL.
FT CARBOHYD 298 298 POTENTIAL.
FT CARBOHYD 452 452 POTENTIAL.
FT CARBOHYD 480 480 POTENTIAL.
FT CARBOHYD 565 565 POTENTIAL.
FT CONFLICT 194 194 R -> A (IN REF. 2).
FT CONFLICT 460 460 T -> I (IN REF. 2).
FT CONFLICT 642 642 A -> G (IN REF. 2).
FT CONFLICT 768 768 N -> I (IN REF. 2).
FT CONFLICT 904 904 S -> T (IN REF. 2).
SQ SEQUENCE 908 AA; 101741 MW; 18865C0F CRC32;
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Query Match 3.4%; Score 232; DB 1; Length 908;  
Best Local Similarity 23.0%; Pred. No. 5,44e-19;

Matches 65; Conservative 96; Mismatches 98; Indels 24; Gaps 21;

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Db 590 VALGII-ATTEVIYVFRNDPIYRASGRELSTYLLGLGIFLSTIFLM-I-AA--PD 644
Qy 487 LTLIGMIMASAFLEFN-INKRNOKLIKMSPPYNNLLIIGMLSTASIFLFDLDSFSE 545
Db 645 -TT-ICSFRRVFLGSGMFSTALLTKNRHRIFEQGRKSTVAPKIFSPASQVITFS 701
Qy 546 KTFETLCYFVTLVGYTTAFGAMFAKTWRVHAIFKNYKMK-K-KIKDKLLIVYGG 602
Db 702 LISVQLGVEVFNVDPHIID-YG-EORTLDPEKA-RGVLK-CDISLST-ICSL-GY 755
Qy 603 MLIDLCILICQAVDPLRRTVERYSMEPDPAGRDISIRPLEHCENHTMTWLGIVAY 662
Db 756 SILLMTY-TYVALKARGVPELFEFNKAPRIGFTMYTTCIIMLAFVPIFGTAQSAEKYI 813
Qy 663 KGLMFGCFL-AMETRNYSIPALNDSKYIGMSYVNWGIMCIIGAASFLTRDQPNVQFC 721
Db 814 OTTLVMSLSASVSLGMLYPKYIILFHPEQNVQKRKSF 856
Qy 722 -YVALVI-I-FCSTITLCLVFVPKLITLTNPDAATQNNRQF 761
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RESULT 5
ID MGR6 HUMAN STANDARD. PRT. 877 AA.
AC 015303:
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 6 PRECURSOR.
GN GRM6 OR MGLUR6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97358610.
RA HASHIMOTO T., INAZAWA J., OKAMOTO N., TAGAMA Y., BESSHO Y., HONDA Y.,
RA NAKANISHI S.;
RT "The whole nucleotide sequence and chromosomal localization of the
RT gene for human metabotropic glutamate receptor subtype 6."
RL Eur. J. Neurosci. 9:1226-1235(1997).
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CC -I- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLYLATE CYCLASE
CC ACTIVITY.
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR4.
CC -----
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CC or send an email to license@isb.slb.ch).
CC -----
DR EMBL: U82083; AAB82068.1; -.
DR GDB: GCR_2607; -.
DR MIM: 604096; -.
DR PROSITE: PS00979; G_PROTEIN_RECP_F3_1; 1.
DR PROSITE: PS00980; G_PROTEIN_RECP_F3_2; 1.
DR PROSITE: PS00981; G_PROTEIN_RECP_F3_3; 1.
DR PFAM: PF00003; 7tm_3; 1.
DR PFAM: PF01094; ANF_receptor; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family; Vision.
FT SIGNAL 1 24
FT CHAIN 25 877
FT DOMAIN 25 585
FT TRANSSEM 586 608
FT DOMAIN 609 622
FT TRANSSEM 623 643
FT DOMAIN 644 654
FT TRANSSEM 655 673
FT DOMAIN 674 697
FT TRANSSEM 698 718
FT DOMAIN 719 748
FT TRANSSEM 749 770
FT DOMAIN 771 783
FT TRANSSEM 784 806
FT DOMAIN 807 819
FT TRANSSEM 820 845
FT DOMAIN 846 877
FT CARBOHYD 296 296
FT CARBOHYD 451 451
FT CARBOHYD 479 479
FT CARBOHYD 567 567
SQ SEQUENCE 877 AA; 95436 MW; D5A6C038 CRC32;
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Query Match 3.3%; Score 225; DB 1; Length 877;  
Best Local Similarity 21.5%; Pred. No. 8,73e-18;

Matches 60; Conservative 91; Mismatches 106; Indels 22; Gaps 19;

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Db 592 LAVLGIVATTYVATVFRNNTPIYRASGRELSTYLLGLIPLIYA-I-TF-L--MVAEP 645
Qy 487 LTLIGMIMASAFLEFNINKRNOKLIKMSPPYNNLLIIGMLSTASIFLFDGDSFSEK 546
Db 646 G-AAVCAARRFLGTSTSYSALLTKTRIRYIFEQGRSTVPPPLSPISQVITTS 704
Qy 547 TFEFTLCYFVTLVGYTTAFGAMFAKTWRVHAIFKNYK--MKK-IIKDKLLIVYGM 603
Db 705 TSLQVVGMIATMGARPHSVID-YE-EORTVDEQA-RGVLK-CDMSLST-IGCL-GY- 757
Qy 604 LLDLCLICQAVDPLRRTVERYSMEPDPAGRDISIRPLEHCENHTMTWLGIVAYK 663
Db 758 SILLMTY-TYVALKARGVPELFEFNKAPRIGFTMYTTCIIMLAFVPIFGTAQSAEKYI 816
Qy 664 GLTMFGCFLAMETRNVSIP-ALNDSKYIGMSYVNWGIMCIIGAASFLTRDQPNVQFC- 721
Db 817 TTTLVMSLSASVSLGMLYPKYIILFHPEQNVQKR 855
Qy 722 YVALVI-I-FCSTITLCLVFVPKLITLTNPDAATQNNR 758
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CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: IS WIDELY DISTRIBUTED IN THE CNS. PREDOMINANT  
 CC EXPRESSION IS SEEN IN THE GRANULE CELLS OF THE CEREBELLUM.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.  
 CC STRONGEST, TO MGUR4.  
 CC  
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 CC  
 CC EMBL: M92077; -; NOT\_ANNOTATED\_CDS.  
 CC EMBL: M90518; AAA93190.1; -;  
 CC PIR: JH0563; JH0563.  
 CC GCRDB: GCR\_0352; -;  
 CC GCRDB: GCR\_0363; -;  
 CC PROSITE: PS00979; G-PROTEIN\_RECEP\_F3\_1; 1.  
 CC PROSITE: PS00980; G-PROTEIN\_RECEP\_F3\_2; 1.  
 CC PROSITE: PS00981; G-PROTEIN\_RECEP\_F3\_3; 1.  
 CC PIRAM: PF00003; 7tm\_3; 1.  
 CC PIRAM: PF01094; ANF\_receptor; 1.  
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
 CC Multi-gene family.  
 CC SIGNAL 1 32  
 CC CHAIN 1 912  
 CC DOMAIN 33 587  
 CC TRANSMEM 588 610  
 CC DOMAIN 611 624  
 CC TRANSMEM 625 645  
 CC DOMAIN 646 656  
 CC TRANSMEM 657 675  
 CC DOMAIN 676 699  
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 CC DOMAIN 721 750  
 CC TRANSMEM 751 772  
 CC DOMAIN 773 785  
 CC TRANSMEM 786 808  
 CC DOMAIN 809 821  
 CC TRANSMEM 822 847  
 CC DOMAIN 848 912  
 CC CARBOHYD 98 98  
 CC CARBOHYD 301 301  
 CC CARBOHYD 454 454  
 CC CARBOHYD 484 484  
 CC CARBOHYD 569 569  
 CC CONFLICT 124 124  
 CC SEQUENCE 912 AA: 101818 MW: 95FEED6 CRC32:  
 Query Match 3.3%; Score 225; DB 1; Length 912;  
 Best Local Similarity 22.6%; Pred. No. 8.73e-18;  
 Matches 65; Conservative 93; Mismatches 101; Indels 29; Gaps 23;

QY 714 DQWVFC-IVALV-I-FCSTITLCVFPKILITLTPDAQONRR 758  
 RESULT 8  
 ID MGR7\_RAT STANDARD; PRT; 915 AA.  
 DT P35400;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE METABOTROPIC GLUTAMATE RECEPTOR 7 PRECURSOR.  
 GN GRM7 OR MGUR7.  
 OS Rattus norvegicus (Rat)  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;  
 RX MEDLINE; 94117433.  
 RA OKAMOTO N., HORI S., AKAZAWA C., HAYASHI Y., SHIGEMOTO R.,  
 RA MIZUNO N., NAKANISHI S.;  
 RT "Molecular characterization of a new metabotropic glutamate receptor  
 RT MGUR7 coupled to inhibitory cyclic AMP signal transduction.";  
 RT J Biol. Chem. 269:1231-1236(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-OLFACTORY BULB;  
 RX MEDLINE; 94195260.  
 RA SAUGSTAD J.A., KINZIE J.M., MULVIHILL E.R., SEGERSON T.P.,  
 RA WESTERROOK G.L.;  
 RT "Cloning and expression of a new member of the L-2-amino-4-  
 RT phosphonobutyric acid-sensitive class of metabotropic glutamate  
 RT receptors.";  
 RT Mol. Pharmacol. 45:367-372(1994).  
 CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR  
 CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLYL CYCLASE  
 CC ACTIVITY.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: WIDELY DISTRIBUTED THROUGHOUT THE BRAIN.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.  
 CC STRONGEST, TO MGUR4.  
 CC  
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 CC  
 CC EMBL: D16817; BAA04092.1; -;  
 CC EMBL: U06832; AAA20655.1; -;  
 CC GCRDB: GCR\_0945; -;  
 CC GCRDB: GCR\_0946; -;  
 CC PROSITE: PS00979; G-PROTEIN\_RECEP\_F3\_1; 1.  
 CC PROSITE: PS00980; G-PROTEIN\_RECEP\_F3\_2; 1.  
 CC PROSITE: PS00981; G-PROTEIN\_RECEP\_F3\_3; 1.  
 CC PIRAM: PF00003; 7tm\_3; 1.  
 CC PIRAM: PF01094; ANF\_receptor; 1.  
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
 CC Multi-gene family; Olfaction.  
 CC SIGNAL 1 32  
 CC CHAIN 33 915  
 CC DOMAIN 33 590  
 CC TRANSMEM 591 615  
 CC DOMAIN 616 627  
 CC TRANSMEM 628 648  
 CC DOMAIN 649 654  
 CC TRANSMEM 655 675  
 CC DOMAIN 676 702  
 CC TRANSMEM 703 723  
 CC DOMAIN 724 753  
 CC TRANSMEM 754 775  
 CC DOMAIN 776 788  
 CC METABOTROPIC GLUTAMATE RECEPTOR 7.  
 CC I (POTENTIAL).  
 CC CYTOPLASMIC (POTENTIAL).  
 CC II (POTENTIAL).  
 CC EXTRACELLULAR (POTENTIAL).  
 CC III (POTENTIAL).  
 CC CYTOPLASMIC (POTENTIAL).  
 CC IV (POTENTIAL).  
 CC EXTRACELLULAR (POTENTIAL).  
 CC V (POTENTIAL).  
 CC CYTOPLASMIC (POTENTIAL).



FT TRANSMEM 789 810 VI (POTENTIAL).  
 FT DOMAIN 811 825 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 826 850 VII (POTENTIAL).  
 FT DOMAIN 851 915 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 98 98 POTENTIAL.  
 FT CARBOHYD 458 458 POTENTIAL.  
 FT CARBOHYD 486 486 POTENTIAL.  
 FT CARBOHYD 572 572 POTENTIAL.  
 SQ SEQUENCE 915 AA; 102231 MW; AF4AD466 CRC32;

Query Match 3.1%; Score 214; DB 1; Length 915;  
 Best Local Similarity 22.9%; Pred. No. 6,48e-16;  
 Matches 65; Conservative 87; Mismatches 106; Indels 26; Gaps 22;

DB 597 LAMGII-ATIFVATPIRYNDPIYASGRELSTVLTGIFLCY--IIF-L--MIA- 648  
 QY 487 LITIGMIMASAFLEFN-IKNRNOKLIKMSPPYNNLLILGMLSTASIFLEGDSFVSE 545  
 DB 649 KPDVAVCSFRFVFLGLGMCISYALTLTKNRIYRIFEOGKRSVAPRLISPTSLATSS 708  
 QY 546 KTEFLCTVPTWILVGTGTAFAGMFAKTWRVHAIFKNVKK-K--KIKDOKLIVYG 602  
 DB 709 LISVOLGVEF-WGVDPNNIID-YD-EHKTMPEQA-RGYLK-CDITDQI-IGSL-G 761  
 QY 603 MLTIDL-CILCOWADVPLRRTYERSMEPDAGDISIRPLEHCENTHTWTWLGIVYA 661  
 DB 762 YSILIMV-TC-TVYAIKTRGVENENAKPIGFTMYTCIYWLAFIPFEGTAQSAEKLY 819  
 QY 662 YKGLIMLFCGLAMETRNVSIPA-LNDSKYIGMSYVNGIMCIIGANVSFLTRDOPVVOF 720  
 DB 820 IOTTLTISMLNSASVALGMLYMPKVIITFHELVNOKRKSF 863  
 QY 721 C-IVALVI-I-FCSTITLCLVFPKLTITLTNDATONRRROF 761

RESULT 9  
 ID MGR7\_HUMAN STANDARD; PRT; 915 AA.  
 AC Q14831;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-DEC-1999 (Rel. 39, Last annotation update)  
 DE METABOTROPIC GLUTAMATE RECEPTOR 7 PRECURSOR.  
 GN GRM7 OR MGLUR7.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RX MEDLINE; 96437220.  
 RA MAKOFF A., PILLING C., HARRINGTON K., EMSON P.;  
 RT "Human metabotropic glutamate receptor type 7: molecular cloning and  
 RT mRNA distribution in the CNS";  
 RL Brain Res. Mol. Brain Res. 40:165-170(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 98141892.  
 RA WU S., WRIGHT R.A., ROCKETT P.K., BURGETT S.G., ARNOLD J.S.,  
 RA ROSECK P.R. JR., JOHNSON B.G., SCHOEPP D.D., BELGARD R.M.;  
 RT "Group III human metabotropic glutamate receptors 4, 7 and 8:  
 RT molecular cloning, functional expression, and comparison of  
 RT pharmacological properties in RGT cells";  
 RL Brain Res. Mol. Brain Res. 53:88-97(1998).  
 CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR  
 CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE  
 CC ACTIVITY.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.  
 CC STRONGEST TO MGLUR4.  
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DR EMBL: X94552; CA64245.1; -  
 DR EMBL: U92458; A851763.1; -  
 DR MIM: 604101; -  
 DR GCRDB; GCR-1890; -  
 DR GCRDB; GCR-2071; -  
 DR PROSITE; PS00979; G-PROTEIN\_RECEP\_F3\_1; 1.  
 DR PROSITE; PS00980; G-PROTEIN\_RECEP\_F3\_2; 1.  
 DR PROSITE; PS00981; G-PROTEIN\_RECEP\_F3\_3; 1.  
 DR PFAM; PF01094; ANF\_receptor; 1.  
 DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
 KW Multigene family; Oligation; Polymorphism.  
 FT SIGNAL 1 32  
 FT CHAIN 33 915  
 FT DOMAIN 33 590  
 FT TRANSMEM 591 615  
 FT DOMAIN 616 627  
 FT TRANSMEM 628 648  
 FT DOMAIN 649 654  
 FT TRANSMEM 655 675  
 FT DOMAIN 676 702  
 FT TRANSMEM 703 723  
 FT DOMAIN 724 753  
 FT TRANSMEM 754 775  
 FT DOMAIN 776 788  
 FT TRANSMEM 789 810  
 FT DOMAIN 811 825  
 FT TRANSMEM 826 850  
 FT TRANSMEM 851 915  
 FT CARBOHYD 98 98  
 FT CARBOHYD 458 458  
 FT CARBOHYD 486 486  
 FT CARBOHYD 572 572  
 FT VARIANT 433 433  
 SQ SEQUENCE 915 AA; 102250 MW; 18278B39 CRC32;

Query Match 3.1%; Score 214; DB 1; Length 915;  
 Best Local Similarity 22.9%; Pred. No. 6,48e-16;  
 Matches 65; Conservative 87; Mismatches 106; Indels 26; Gaps 22;

DB 597 LAMGII-ATIFVATPIRYNDPIYASGRELSTVLTGIFLCY--IIF-L--MIA- 648  
 QY 487 LITIGMIMASAFLEFN-IKNRNOKLIKMSPPYNNLLILGMLSTASIFLEGDSFVSE 545  
 DB 649 KPDVAVCSFRFVFLGLGMCISYALTLTKNRIYRIFEOGKRSVAPRLISPTSLATSS 708  
 QY 546 KTEFLCTVPTWILVGTGTAFAGMFAKTWRVHAIFKNVKK-K--KIKDOKLIVYG 602  
 DB 709 LISVOLGVEF-WGVDPNNIID-YD-EHKTMPEQA-RGYLK-CDITDQI-IGSL-G 761  
 QY 603 MLTIDL-CILCOWADVPLRRTYERSMEPDAGDISIRPLEHCENTHTWTWLGIVYA 661  
 DB 762 YSILIMV-TC-TVYAIKTRGVENENAKPIGFTMYTCIYWLAFIPFEGTAQSAEKLY 819  
 QY 662 YKGLIMLFCGLAMETRNVSIPA-LNDSKYIGMSYVNGIMCIIGANVSFLTRDOPVVOF 720  
 DB 820 IOTTLTISMLNSASVALGMLYMPKVIITFHELVNOKRKSF 863  
 QY 721 C-IVALVI-I-FCSTITLCLVFPKLTITLTNDATONRRROF 761  
 RESULT 10  
 ID MGR5\_RAT STANDARD; PRT; 1203 AA.  
 AC P31424;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-DEC-1999 (Rel. 39, Last annotation update)

FT	DOMAIN	827	1203	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	88		POTENTIAL.
FT	CARBOHYD	209	209	POTENTIAL.
FT	CARBOHYD	377	377	POTENTIAL.
FT	CARBOHYD	381	381	POTENTIAL.
FT	CARBOHYD	444	444	POTENTIAL.
FT	CARBOHYD	733	733	POTENTIAL.
FT	VARSPLIC	876	907	MISSING (IN ISOFORM 5A).
SO	SEQUENCE	1203 AA:	131885 MW; 29555EA33 CMC32;	
Query Match				
Best Local Similarity 3.1%; Score 215; DB 1; Length 1203;				
Matches 54; Conservative 57; Mismatches 61; Indels 19; Gaps 17				
Db	655	AMSYALATYTKNPIHILLAGSK-KKICTKRPMSCA-QLVIAF-ILIC---IO-LGI 707		
Qy	564	TLAFGPAKTRVHAFENYANKRKRIKQKILVYGSMLIDLCILHOMVDPRLRT 623		
Db	708	VALFTEPDDIMHDYSIREVYLICNTNLCV-VPEL-GYNGLLIL-SCFFAFKTRNP 764		
Qy	624	VERSEMEDEPAGSDI-SIPLEHEENTHMTILGLVAYKGLMLGCG-FLAMETRRNS 681		
Db	765	-ANFEAFIAFTMYTCIMWLAEPVI-YEGSNYKILITMCF-S-VSL-SATVALGCM-FV 818		
Qy	682	IPALDSKYSIGMSYVWIMCIGIAVSEFLRDPQWQVCIAVLAIFCSTITL-CLVRF 740		
Db	819	PRVYITLAKPE 829		
Qy	741	PKLITRTNP 751		
RESULT 11				
ID	MGR5_HUMAN	STANDARD;	PRT;	1212 AA.
AC	P41594;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-OCT-1996 (Rel. 34, last sequence update)			
DT	15-DEC-1999 (Rel. 39, last annotation update)			
DE	METABOTROPIC GLUTAMATE RECEPTOR 5 PRECURSOR.			
GN	GRM5 OR MGLUR5.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Primates; Catarrhini; Homidae; Homo.			
OC	[1]			
RP	SEQUENCE FROM N.A.			
RP	TISSUE-BRAIN;			
RC	MEDLINE: 94197696.			
RA	MINAKAMI R., KATSUKI F., YAMAMOTO T., NAKAMURA K., SUGIYAMA H.;			
RA	KATSUKI F.;			
RA	Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE OF 860-952 FROM N.A.			
RC	TISSUE-BRAIN;			
RC	MEDLINE: 93343913.			
RA	MINAKAMI R., KATSUKI F., SUGIYAMA H.;			
RT	"A variant of metabotropic glutamate receptor subtype 5: an			
RL	evolutionally conserved insertion with no termination codon."			
CC	Biochem. Biophys. Res. Commun. 194:622-627(1993).			
CC	- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS			
CC	IS MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-			
CC	MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-			
CC	CALCIUM SECOND MESSENGER SYSTEM AND GENERATES A CALCIUM-ACTIVATED			
CC	CHLORIDE CURRENT.			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-1- ALTERNATIVE PRODUCTS: TWO ISOFORMS, 5A (SHOWN HERE) AND 5B; ARE			
CC	PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER BY AN INSERTION OF			
CC	32 RESIDUES.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.			
CC	STRONGEST, TO MGLUR1.			

```
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CC -----
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DR EMBL; D28538; BAA05891.1; -
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DR EMBL; D28539; BAA05892.1; -
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DR EMBL; S64316; AADI3954.1; -
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DR GCRDB; GCR_0761; -
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```
DR GCRDB; GCR_1002; -
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```
DR GCRDB; GCR_1003; -
```

```
DR GCRDB; GCR_1317; -
```

```
DR MIM; 604102; -
```

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DR PROSITE; PS00979; G_PROTEIN_RECPEP_F3_1; 1.
```

```
DR PROSITE; PS00980; G_PROTEIN_RECPEP_F3_2; 1.
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```
DR PROSITE; PS00981; G_PROTEIN_RECPEP_F3_3; 1.
```

```
DR PFAM; PF00003; 7tm_3; 1.
```

```
DR PRAM; pf01094; ANF_receptor; 1.
```

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KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
```

```
KW Multigene family; Alternative splicing.
```

```
FT SIGNAL 1 20
```

```
FT CHAIN 1 1212
```

```
FT DOMAIN 21 579 METABOTROPIC GLUTAMATE RECEPTOR 5.
```

```
FT DOMAIN 22 579 I (POTENTIAL).
```

```
FT TRANSMEM 580 602 CYTOPLASMIC (POTENTIAL).
```

```
FT DOMAIN 603 616 POTENTIAL.
```

```
FT TRANSMEM 617 637 II (POTENTIAL).
```

```
FT DOMAIN 638 648 EXTRACELLULAR (POTENTIAL).
```

```
FT TRANSMEM 649 667 III (POTENTIAL).
```

```
FT DOMAIN 668 693 CYTOPLASMIC (POTENTIAL).
```

```
FT TRANSMEM 694 714 IV (POTENTIAL).
```

```
FT DOMAIN 715 737 EXTRACELLULAR (POTENTIAL).
```

```
FT TRANSMEM 738 759 V (POTENTIAL).
```

```
FT DOMAIN 760 772 CYTOPLASMIC (POTENTIAL).
```

```
FT TRANSMEM 773 793 VI (POTENTIAL).
```

```
FT DOMAIN 796 801 EXTRACELLULAR (POTENTIAL).
```

```
FT TRANSMEM 802 827 VII (POTENTIAL).
```

```
FT DOMAIN 828 1212 CYTOPLASMIC (POTENTIAL).
```

```
FT CARBOHYD 88 88 POTENTIAL.
```

```
FT CARBOHYD 210 210 POTENTIAL.
```

```
FT CARBOHYD 378 378 POTENTIAL.
```

```
FT CARBOHYD 382 382 POTENTIAL.
```

```
FT CARBOHYD 445 445 POTENTIAL.
```

```
FT CARBOHYD 734 734 POTENTIAL.
```

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FT VARSPPLIC 877 908 MISSING (IN ISOFORM 5A).
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SQ SEQUENCE 1212 AA; 132468 MW; 16E81574 CMC3;
```

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Query Match 3.1%; Score 215; DB 1; Length 1212;
```

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Best Local Similarity 28.3%; Pred. No. 4,39e-16;
```

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Matches 54; Conservative 57; Mismatches 61; Indels 19; Gaps 17;
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```
Db 656 AMSYSLATYTKNRIARILASGK-KKICTKKPRMSACA-QLVIAF-IILC--IG-IGII 708  
::: : : : : : | | | : : : : : : : : : : : : : : : : : : : : :  
Oy 554 TTAGCAMFAKRWKHAIFKNVKKKKIKINDOKLLIVYGSMLLDICILLICMGANDPLART 623  
::: : : : : : : : : : : : : : : : : : : : : : : : : : : :  
Db 709 VALEFMPEPDIMHDPISIREVYLICNTNLGV-VTPL-GYNGLLI-SCTFYAFETRNVP 765  
| : ||| : | ||| : | : : : : : : : : : : : : : : : : : : : : :  
Oy 624 VERYSMEEDPPAGRDI-SIRPLLEHCENHTMTWLGIYAAYKGLMFGC-FLAWETRNVSS 681  
: : : : : : : : : : : : : : : : : : : : : : : : : : : :  
Db 766 -ANFEAKYIAFWYTTCIIMLAFPVR-YGNSYKLIITMCF-S-VSL-SATVALGCM-FV 819  
: : : : : : : : : : : : : : : : : : : : : : : : : : : :  
Oy 662 IPALDSKTISMYSNYNGIMCIIGAASFILTRQPNOVCIVALVAIIFCSITTL-CLVFV 740  
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
Db 820 PKVYIIILAKE 830  
|| : : : :  
Oy 741 PKLIPLRTNP 751
```

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RESULT 12 STANDARD; PRT; 976 AA.  
ID MGR_DROME
```

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AC P91685; (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE METABOTROPIC GLUTAMATE RECEPTOR PRECURSOR.
GN GLUR4 OR GLU-RA.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidae; Drosophilidae; Drosophila.
NC [1]
RP SEQUENCE FROM N.A..
RC STRAIN=OREGON-R;
RX MEDLINE: 96421661.
RA PARENTIER M.L., PIN J.P., BOCKAERT J., GRAU Y.;
RT "Cloning and functional expression of a Drosophila metabotropic
RT glutamate receptor expressed in the embryonic CNS.";
RL J. Neurosci. 16:6687-6694(1996).
CC -I- FUNCTION: RECEPTOR FOR GLUTAMATE.
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I- DEVELOPMENTAL STAGE: EXPRESSED IN THE CNS OF THE LATE EMBRYO.
CC -I- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X99675; CAA67993.1; -.
CC GCRDB: GCR_1123; -.
DR DRLYBASE; FBgn0019985; Glu-RA.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PFAM; PF00003; 7tm_3; 1.
DR PFAM; PF01094; ANF_receptor; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 ?
FT CHAIN ? 976 METABOTROPIC GLUTAMATE RECEPTOR.
FT DOMAIN ? 626 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 627 649 I (POTENTIAL).
FT DOMAIN 650 663 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 664 685 II (POTENTIAL).
FT DOMAIN 685 695 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 696 714 III (POTENTIAL).
FT DOMAIN 715 738 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 739 759 IV (POTENTIAL).
FT DOMAIN 760 782 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 783 804 V (POTENTIAL).
FT DOMAIN 805 817 VI (POTENTIAL).
FT TRANSMEM 818 840 VI (POTENTIAL).
FT DOMAIN 841 850 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 851 876 VII (POTENTIAL).
FT DOMAIN 877 976 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 112 112 POTENTIAL.
FT CARBOHYD 143 143 POTENTIAL.
FT CARBOHYD 216 216 POTENTIAL.
FT CARBOHYD 299 299 POTENTIAL.
FT CARBOHYD 386 386 POTENTIAL.
FT CARBOHYD 491 491 POTENTIAL.
FT CARBOHYD 524 524 POTENTIAL.
SQ SEQUENCE 976 AA; 10845 MW; 56A0DD94 CRC32;

Query Match 3.0%; Score 210, DB 1; Length 976;
Best Local Similarity 24.7%; Pred. No. 3,05e-15;
Matches 69; Conservative 90; Mismatches 91; Indels 29; Gaps 21;

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FT TRANSMEM      613    635          I (POTENTIAL).
ET DOMAIN        638    649       CYTOSOLASMIC (POTENTIAL) .
FT TRANSMEM     650    670         II (POTENTFL) .
ET DOMAIN        671    681       EXTRACELLULAR (POTENTIAL) .
FT TRANSMEM     682    700         III (POTENTIAL) .
ET DOMAIN        701    724       CYTOPLASMIC (POTENTIAL) .
FT TRANSMEM     725    745       IV (POTENTIAL) .
ET DOMAIN        746    769       EXTRACELLULAR (POTENTIAL) .
FT TRANSMEM     770    792       V (POTENTIAL) .
ET DOMAIN        793    805       CYTOPLASMIC (POTENTIAL) .
FT TRANSMEM     806    828       VI (POTENTIAL) .
ET DOMAIN        829    836       EXTRACELLULAR (POTENTIAL) .
FT TRANSMEM     837    862       VII (POTENTIAL) .
ET DOMAIN        863    1079      CYTOSOLASMIC (POTENTIAL) .
FT CARBOHYD     90    90          POTENTIAL.
FT CARBOHYD     130   130          POTENTIAL.
FT CARBOHYD     261   261          POTENTIAL.
FT CARBOHYD     287   287          POTENTIAL.
FT CARBOHYD     386   386          POTENTIAL.
ET CARBOHYD     446   446          POTENTIAL.
ET CARBOHYD     468   468          POTENTIAL.
ET CARBOHYD     488   488          POTENTIAL.
FT CARBOHYD     541   561          POTENTIAL.
FT CARBOHYD     594   594          POTENTIAL.
SQ SEQUENCE      1079 AA; 120867 MW; 34118BE9 CRC32;.


Query Match               2.9%; Score No. DB 1; Length 1079;
Best Local Similarity 29.7%; Pred. No. 2.04e-13;
Matches 27; Conservative 30; Mismatches 34; Indels 0; Gaps 0;


Db      125 LDFCNCSHIPSTIAVVGATSGSVATANLGLFPIQPVYASSSRLSKNKOYSKFL 184
Oy      113 LAFYDAIKRYGNHNLMTVEFGCVPSVTSLAESIQGNNLVLSFAATTPTVLADKKRPYYE 172
Db      185 RTIPNDHQATAADIIEFRWNWGTIAD 215
Oy      173 RIVPSDNVANVPAILKLKHRRRVRGETLTOD 203


RESULT 14
ID MGR2_HUMAN STANDARD; PRT: 872 AA.
AC Q14A16;
DT 01-NOV-1997 (Rel. 35, Created)
DI 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-DEC-1999 (Rel. 39, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 2 PRECURSOR.
GM GRM2 OR MGJUR2.
OS Homo sapiens (Human) .
OC Eukaryota; Metazoa; Chordata; Vertebrat; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoideae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95346007.
RA FLOR P.J., LINDAUER K., PUTTNER I., RUEGG D., LUHK S., KNOPPEL T.,
RA KUHN R.;
RA "Molecular cloning, functional expression and pharmacological
RT characterization of the human metabotropic glutamate receptor type
RT 2."
RL Eur. J. Neurosci. 7:622-629(1995).
CC - FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS
CC MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE ACTIVITY.
CC MAY IMMEDIATE SUPPRESSION OF NEUROTRANSMISSION OR MAY BE INVOLVED IN
CC SYNAPTOGENESIS OR SYNAPTIC STABILIZATION.
CC - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC - TISSUE SPECIFICITY: WIDELY EXPRESSED IN DIFFERENT REGIONS OF THE
CC ADULT BRAIN AS WELL AS IN FETAL BRAIN.
CC - SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONEST, TO MLDR3.
-----
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CC -----

DR EMBL: L35318; AAA76855.1; -

DR GCRDB: GCR1846; -

DR MIM: 604099; -

DR PROSITE: PS00979; G-PROTEIN\_RECEP\_F3\_1; 1.

DR PROSITE: PS00980; G-PROTEIN\_RECEP\_F3\_2; 1.

DR PROSITE: PS00981; G-PROTEIN\_RECEP\_F3\_3; 1.

DR PIRAM: PF00003; 7tm3; 1.

DR PIRAM: PF01094; ANF\_receptor; 1.

KM G-protein coupled receptor; Transmembrane; Glycoprotein; Signal; Multi-gene family.

FT SIGNAL 1 18

FT CHAIN 19 872

FT DOMAIN 19 567

FT TRANSMEM 568 590

FT DOMAIN 591 604

FT TRANSMEM 605 625

FT DOMAIN 626 636

FT TRANSMEM 637 653

FT DOMAIN 656 679

FT TRANSMEM 680 700

FT DOMAIN 701 725

FT TRANSMEM 726 747

FT DOMAIN 748 760

FT TRANSMEM 761 783

FT DOMAIN 784 793

FT TRANSMEM 794 819

FT DOMAIN 820 872

FT CARBOHYD 203 203

FT CARBOHYD 286 286

FT CARBOHYD 338 338

FT CARBOHYD 402 402

FT CARBOHYD 547 547

SO SEQUENCE 872 AA; 95507 MR; 9369084C CRC32;

Query Match 2.8%; Score 193; DB 1; Length 872;

Best Local Similarity 24.2%; Pred. No. 1,95e-12;

Matches 54; Conservative 69; Mismatches 78; Indels 22; Gaps 19;

DB 611 GGATLCMFFFLA-KPSTAVCTLRIGTAFSVCSALTKTRIKRTGAREGAG 669

Y 531 ASIFL-EGLDGSEVSEKFTETLCTVRLVGYTAFGAFKTRVRAIKRVK--MK 587

DB 670 RPRISASQVAICLALISGOLIVAVMLVVEA-PGT-GK-ETAPER--REV-V-TL--R 720

Y 588 K-KIKOKKLVIVGKMLDLDCILICQAVDPLRTVERYSKPPADISIRPLEH 646

DB 721 CNHRDASM-LGSL-ANVLLIAL-CLLYAFNTRKCP-ENFNEAKFTGFTMTTCIIITIAL 776

Y 647 CENHMTIMWIGIYAVYKGLMLFGCEFL-AMETRNVSIPALNDSKYIGMSVYVNGICIG 705

DB 777 LPIFYVSSDYVQVTMCVSVSLSGSVYVGL-FAPKLHII 818

Y 706 AAVSFITRDQPNVQFCIVALLVIFCSIITL-CLVYFVKL-ITL 746

RESULT 15

ID CASR\_HUMAN STANDARD; PRT: 1078 AA.

AC P41180; Q13912; Q16379; Q16108; Q16109; Q16110;

DT 01-FEB-1995 (Rel. 31, Created)

DT 13-NOV-1995 (Rel. 32, Last sequence update)

DT 13-JUL-1999 (Rel. 38, Last annotation update)

DE EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL CALCIUM-SENSING RECEPTOR).

GN CASR OR PCAR1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CC [1]

RN SEQUENCE FROM N.A.

RA PEARCE S.H.S., THAKKER R.V.;

RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE-PARATHYROID;

RX MEDLINE: 95279439.

RA GARRETT J.E., CAPUANO I.V., HAMMERLAND L.G., HUNG B.C., BROWN E.M.,

RA HERBERT S.C., NEMETH E.F., FULLER F.;

RT Molecular cloning and functional expression of human parathyroid

RT calcium receptor cDNAs.;

RL J. Biol. Chem. 270:12919-12925(1995).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE-KIDNEY;

RX MEDLINE: 95408281.

RA AIDA K., KOISHI S., TAWATA M., ONAYA T.;

RT Molecular cloning of a putative Ca(2+)-sensing receptor cDNA from

RT human kidney.;

RL Biochem. Biophys. Res. Commun. 214:524-529(1995).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE: 96343808.

RA FREICHEL M., ZINK-LORENZ A., HOLLOSCHI A., HAFNER M., FLOCKERZI V.,

RA RAUE F.;

RT Expression of a calcium-sensing receptor in a human medullary

RT thyroid carcinoma cell line and its contribution to calcitonin

RT secretion.;

RL Endocrinology 137:3842-3848(1996).

RN [5]

RP VARIANTS FHH GLU-185; LYS-297 AND TRP-795.

RX MEDLINE: 94094324.

RA POLIAK M.R., BROWN E.M., CHOU Y.H., HERBERT S.C., MARX S.J.,

RA SEIDMAN J.G., LEVI T., SEIDMAN C.E., SEIDMAN J.G.;

RT Mutations in the human Ca(2+)-sensing receptor gene cause familial

RT hypocalcemic hypercalcaemia and neonatal severe

RT hyperparathyroidism.;

RL Cell 75:1297-1303(1993).

RN [6]

RP VARIANT ADH ALA-127.

RX MEDLINE: 95179179.

RA POLIAK M.R., BROWN E.M., ESTEP H.L., MCCLAIN P.N., KIFOR O., PARK J.,

RA HERBERT S.C., SEIDMAN C.E., SEIDMAN J.G.;

RT Autosomal dominant hypocalcaemia caused by a Ca(2+)-sensing receptor

RT gene mutation.;

RL Nat. Genet. 8:303-307(1994).

RN [7]

RP VARIANTS FHH MET-62; CYS-66; MET-138; GLU-143 AND GLN-227.

RX MEDLINE: 95243222.

RA CHOU Y.H.W., POLIAK M.R., BRANDI M.L., TOSS G., ARNOVIST H.,

RA ATKINSON A.B., PAPADOULOS S.E., MARX S., BROWN E.M., SEIDMAN J.G.,

RA SEIDMAN C.E.;

RT Mutations in the human Ca(2+)-sensing-receptor gene that cause

RT familial hypocalcemic hypercalcaemia.;

RL Am. J. Hum. Genet. 56:1075-1079(1995).

RN [8]

RP SEQUENCE OF 1-61 FROM N.A., AND VARIANT FHH ALA-39.

RX MEDLINE: 95403641.

RA AIDA K., KOISHI S., INOUE M., NAKAZATO M., TAWATA M., ONAYA T.;

RT Familial hypocalcemic hypercalcaemia associated with mutation in the

RT human Ca(2+)-sensing receptor gene.;

RL J. Clin. Endocrinol. Metab. 80:2594-2598(1995).

RN [9]

RP VARIANTS NSHPT LEU-227 AND TYR-598.

RX MEDLINE: 96292293.

RA PEARCE S.H.S., TRUMP D., WOODING C., BESSER G.M., CHEW S.L.,

RA GRANT D.B., HERTH D.A., HUGHES I.A., PATERSON C.R., WHYTE M.P.,

RA THAKKER R.V.;

RT Calcium-sensing receptor mutations in familial benign hypercalcaemia

RT and neonatal hyperparathyroidism.;

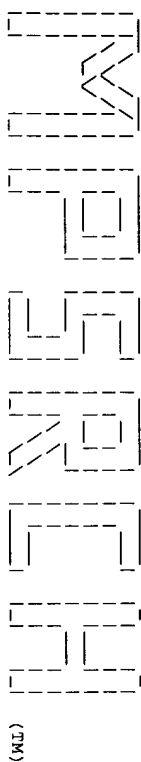
RL J. Clin. Invest. 96:2683-2692(1995).

RN [10]

RP VARIANTS ADHP THR-116; HIS-681 AND SER-806, AND VARIANT SER-851.

RX MEDLINE: 96311554.





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Mpsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Mar 15 21:55:28 2000; MasPar time 64.25 seconds

Tabular output not generated. 690.163 Million cell updates/sec

Title: >US-09-211-755-4  
Description: (1-940) from US09211755.pep  
Perfect Score: 6906  
Sequence: 1 MASPPSSGQPPPPPPPPPPA.....TASPRHRHVPSPFRWVWSGL 940

Scoring table: PAM 150  
Gap 11

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: p1r62  
1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 55.689; Variance 124.230; scale 0.448

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1658	24.0	960	2 JE0356	gamma-aminobutyric ac	2.79e-273
2	1240	3.5	908	2 I49142	metabotropic glutamat	3.04e-17
3	236	3.4	871	2 A46742	metabotropic glutamat	1.23e-16
4	225	3.3	912	2 I58149	metabotropic glutamat	5.49e-15
5	225	3.3	912	2 JH0563	metabotropic glutamat	5.49e-15
6	214	3.1	915	2 A49874	metabotropic glutamat	2.32e-13
7	216	3.1	940	2 T02740	metabotropic protein	1.18e-13
8	215	3.1	1171	2 A42916	metabotropic glutamat	1.66e-13
9	215	3.1	1180	2 J02132	metabotropic glutamat	1.66e-13
10	215	3.1	1212	2 UC2131	metabotropic glutamat	1.66e-13
11	197	2.9	1078	2 S49341	calcium-sensing recep	6.71e-11
12	199	2.9	1079	2 I59362	calcium/polyvalent ca	3.47e-11
13	190	2.8	898	2 T05099	hypothetical protein	6.58e-10
14	194	2.8	1078	2 A56715	calcium receptor (clo	1.79e-10
15	192	2.8	1085	2 S40476	Ca(2+)-sensing recept	3.44e-10
16	194	2.8	1088	2 B56715	calcium receptor (clo	1.79e-10
17	186	2.7	872	2 JH0561	metabotropic glutamat	2.40e-09
18	188	2.7	879	2 JH0562	metabotropic glutamat	1.26e-09
19	178	2.6	1199	2 A41939	G protein-coupled glu	3.07e-08
20	180	2.6	1218	2 S71376	glutamate receptor ho	1.63e-08
21	164	2.4	986	1 OYURGA	speract receptor prec	2.37e-06
22	165	2.4	1108	2 B55915	guanylate cyclase (EC	1.75e-06
23	154	2.2	1325	1 A36699	guanylate cyclase (EC	4.79e-05

24	148	2.1	373	2 A36125	branched-chain amino	2.78e-04
25	144	2.1	938	2 T01809	hypothetical protein	8.78e-04
26	146	2.1	958	2 T02741	hypothetical protein	4.95e-04
27	142	2.1	1005	2 S33525	guanylate cyclase (EC	1.55e-03
28	145	2.1	1125	1 OYURCP	speract receptor prec	6.60e-04
29	136	2.0	1679	2 T15968	hypothetical protein	8.33e-03
30	134	1.9	430	2 H69955	conserved hypothetical	1.44e-02
31	132	1.9	535	2 A54155	natriuretic peptide r	2.49e-02
32	130	1.9	536	2 S71332	natriuretic peptide c	4.28e-02
33	129	1.9	536	2 A45409	atrial natriuretic pe	5.59e-02
34	129	1.9	537	1 A28111	natriuretic peptide r	5.59e-02
35	128	1.9	637	2 C65129	hypothetical ABC tran	7.30e-02
36	130	1.9	1103	2 UCS581	guanylate cyclase (EC	4.28e-02
37	132	1.9	1108	2 I59385	guanylate cyclase (EC	2.49e-02
38	124	1.8	358	2 B69826	hypothetical protein	2.09e-01
39	125	1.8	404	1 LABECA	latent membrane prote	1.61e-01
40	126	1.8	540	1 OYHUCR	natriuretic peptide r	1.24e-01
41	125	1.8	662	2 DA0228	neurexin II-beta prec	1.61e-01
42	124	1.8	676	2 OY0084	myosin heavy chain, f	2.09e-01
43	126	1.8	1047	1 OYRTBR	atrial natriuretic pe	1.24e-01
44	124	1.8	1065	2 G72330	hypothetical protein	2.09e-01
45	123	1.8	1937	2 I38055	myosin heavy chain, p	2.72e-01

## ALIGNMENTS

RESULT 1  
ENTRY JE0356 #type complete  
TITLE gamma-aminobutyric acid receptor B precursor - human  
ALTERNATE\_NAMES GABA(B) receptor  
ORGANISM Homo sapiens #common\_name man  
DATE 05-Feb-1999 #sequence\_revision 05-Feb-1999 #text\_change 12-Feb-1999

ACCESSIONS  
REFERENCE JE0356  
#authors Grifa, A.; Totaro, A.; Rommens, J.M.; Carella, M.; Roetto,  
A.; Borgato, L.; Zelante, L.; Gasparini, P.  
#journal Biochem. Biophys. Res. Commun. (1998) 250:240-245  
#title GABA (gamma-amino-butyric acid) neurotransmission:  
Identification and fine mapping of the human GABAB receptor  
gene.

#cross-references MUID:98440782

#accession JE0356  
#molecule\_type mRNA  
#residues 1-960 #label GRI#cross-references GB:Y11044; NID:q2826760  
##note this ORF is not annotated in Genbank entry HSGTHA1,  
release 109

## GENETICS

#map\_position 6p21.3-6p21.3  
KEYWORDS glycoprotein; neurotransmitter receptor; transmembrane  
protein

## FEATURE

1-11  
1-960  
590-613 #domain transmembrane #status predicted #label TM1\  
629-654 #domain transmembrane #status predicted #label TM2\  
666-687 #domain transmembrane #status predicted #label TM3\  
709-730 #domain transmembrane #status predicted #label TM4\  
767-788 #domain transmembrane #status predicted #label TM5\  
803-825 #domain transmembrane #status predicted #label TM6\  
831-856 #domain transmembrane #status predicted #label TM7\  
23,83,439,481,501,  
513,630 #binding site carbohydrate (Asn) (covalent) #status  
predicted

SUMMARY #length 960 #molecular-weight 108148 #checksum 3766

Query Match 24.0%; Score 1658; DB 2; Length 960;

Best local Similarity 36.0%; Pred. No. 2.79e-273;

Matches 248; Conservative 177; Mismatches 247; Indels 16; Gaps 14;

DB 184 GQACGAVAEALAEVDSRDIIPDYELKLHDSKCDPCQAKLYLELLYNPIIILMP 243

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QY 73 GRGLVPEVLAIRQIRNE-SLIRPYFLDLRLYDTECDNAKGLAFDAIKYGNHLMWVG 131
Db 244 G-CSSVSTVAEAAARMNLLVLSYSSPALSNRORPPEFRHPATILNPRVLEFK 302
QY 132 GVCPSVSTIAESIQGNLVLSFAATTPVLAKKKYPIFFKRVDPDANVPAILLKH 191
Db 303 GKKKATLTIQOTTEVTSTLDLEERKENGIBITFROSFFSDPAVYNKLKRODARIIV 362
QY 192 FRRRRVGTLLQDQRFSEVENDLTGLVYGEDIDISDTESNDPCSVKKIKGNDRILL 251
Db 363 GLYEYFARVCEYKERLFKKYVWELGLWADWWF-KIY-DP-SINCYDENTEAIVE 419
QY 252 GQPDQNNAAVFFCAFESEFSGKYQWILPGWEPAWMDQVHEANSSCLRSLLAAME 311
Db 420 GHITTEIYMLNPANTRSISNMTSQEVEKTLKLRHPERTGGFOCAPALAYALALAA 479
QY 312 GYGVDFEPLSSKOITISKTPQOY-EREYNS-KRSGVPSKFFH-G-YAIDGIMYIAKT 367
Db 480 LAKTSGG--GGRSGVRLEDFNNQTTDQIYRANSSSEFEGVSGHVVDASGSRMAWTL 537
QY 368 LQRAMETLHASSRHRIODFNYTDHTLGLKILANAMETNFFGTGGVVF-RNGERGTIK 426
Db 538 IEQPOGSKYKIGYDSTDDLSW-SKTDKMGSGPPADQTVIKTFRLSQKFLISYV 596
QY 427 FTQFQDSREKVGSEYNAVADTLEITINDTIRFQSGSEPPKDKTIIQLRKISDPLYSLSA 486
Db 597 LSSLGIVLAVVCLSFNINYSHVAYIIONSPNLNLTAVCSALAAVFLGLDGHIGRN 656
QY 487 LTLIGIMASAFLEFNKRNOKLIKMSPPYNNLLILOGMLSYASIFLFGDGSFVSRK 546
Db 657 QPFVQOARMLLIGLFGSLGYSMTFKIWWHTGFTKKEKKEMWRTLEPWLVAVTGLL 716
QY 547 TETFLCTVFTWLTGVYTTAFGMAFKATWRVHAIF--KNVKRK-KKIIDQKILVIVGM 603
Db 717 VGMADVLTIAIMOVDPLHRTIETFAKEEPEKDIDVSLIPOLHCSRKNTWLGIFYCYK 776
QY 604 LILDLICILMQAVDPLRRTVERYSMEPPAGRDISTIRPLEHCETHHTWLGIVAYK 663
Db 777 GLLILGILVAVETKSVSTEKINDHRAVMAIYNAVLCLITAPYTMILSSQDAAFAFA 836
QY 664 GLMLTFGCFLAWETRNVSIPALNDSKYIGMSYVNGVICIIGAANSFLTRQPNVQFIV 723
Db 837 SLAIVSSYITLVLPVKMRRLIRGE 864
QY 724 ALVILFCSTTLCLVFPVKRLITLRTPD 751

RESULT 2
ENTRY 149142 #type complete
TITLE metabotropic glutamate receptor 8 - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
ACCESSIONS 149142
#authors Duvoisin, R.M.; Zhang, C.; Ramonell, K.
#journal J. Neurosci. (1995) 15:3075-3083
#title A novel metabotropic glutamate receptor expressed in the retina and olfactory bulb.
#cross-references MUID:95239344
#accession 149142
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-908 ##label RES
#cross-references EMBL:U17252; NID:g854728; PIDN:AAA6149.1;
PDB:g854729
GENETICS
#gene mGluR8
CLASSIFICATION #superfamily metabotropic glutamate receptor 4
KEYWORDS neurotransmitter receptor
SUMMARY #length 908 #molecular_weight 101413 #checksum 2996
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Best Local Similarity 21.8%; Pred. No. 3,04e-17;
Matches 63; Conservative 100; Mismatches 101; Indels 25; Gaps 22;

Db 584 AAVPVLAILGII-ATFEVITFEVRYNDPTVRASGRELSSVLLTGLCYSTIFLM-I- 640
QY 482 SILSAL-TILGIMASAFLEFN-INKNOKLIKMSPPYNNLLILOGMLSYASIFLFGD 539
Db 641 AA--PD-TI--ICGFRILFLGLKCSYALALKTKNRHIREFOGKSVTAPKFSPASQ 695
QY 540 GSEVSEKTFETLCTVRWLTGVYTTAFGMAFKATWRVHAIFKNVKK-K-KIKDOKL 596
Db 696 LVTFSLISVOLGCVFVFWVDPPHTIID-YG-EQRTIDPE-NARGVLR-CQDSIDL-I 750
QY 597 LVYIGMLLIDCLICMQAVDPLRRTVERYSMEPPAGRDISTIRPLEHCETHHTWLG 656
Db 751 CSL-GYSILMW-TC-TVYAIKTRGVPEFNEAKPIGFTWYTCIILWAFIPFEGTAOS 807
QY 657 GIYVAYKGLMLTFGCFLAWETRNVSIP-ALNDSKYIGMSYVNGVICIIGAANSFLTRDQ 715
Db 808 AEKMYIOTTLTVMSLSASVSGMLKMPKVIITIHPEQNOVKRRKSF 856
QY 716 PNVQFC-IVALVI-I-FCSTTLCLVFPVKRLITLRTPDPAATQNRROF 761

RESULT 3
ENTRY A46742 #type complete
TITLE metabotropic glutamate receptor, mGluR6 - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Sep-1999
ACCESSIONS A46742
#authors Nakajima, Y.; Iwakabe, H.; Akazawa, C.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi, S.
#journal J. Biol. Chem. (1993) 268:11868-11873
#title Molecular characterization of a novel retinal metabotropic glutamate receptor mGluR6 with a high agonist selectivity for L-2-amino-4-phosphonobutylate.
#cross-references MUID:93280152
#accession A46742
#status preliminary
#molecule_type nucleic acid
#residues 1-871 ##label NAK
#cross-references GB:D13963; NID:g391856; PIDN:BA03066.1;
PID:d1003572; PID:g391857
#experimental_source retina
#note sequence extracted from NCBI backbone (NCBI:133246, NCBI:133250)
CLASSIFICATION #superfamily metabotropic glutamate receptor 4
KEYWORDS G protein-coupled receptor; transmembrane protein
SUMMARY #length 871 #molecular_weight 95088 #checksum 3942

Query Match 3.4%; Score 236; DB 2; Length 871;
Best Local Similarity 22.9%; Pred. No. 1,23e-16;
Matches 64; Conservative 90; Mismatches 102; Indels 24; Gaps 21;

Db 586 LAVIG-IMATTTIMAFMHNPTVRASGRELSSVLLTGLFIYA-I-TF-L--MYAE 638
QY 487 LTLIGIMASAFLEFNKRNOK-LIKMSPPYNNLLIIGMLSYASIFLFGDGSFVSE 545
Db 639 PC-AAICARRLILGTTLSALLTKTNRYRIFEDGKRSVPPPIPSPTSLQVITFG 697
QY 546 KTFEELCTVFTWLTGVYTTAFGMAFKATWRVHAIFKNVK--MKKK-IIKKQKLLVYGG 602
Db 698 LLSLVQVGVYIANLGAQPPSVLD-YE-EQRTYDPA-QRGVLR-CQDSDLSL-IGCL-GY 751
QY 603 MLTIDLCILICMQAVDPLRRTVERYSMEPPAGRDISTIRPLEHCETHHTWLGIVAY 662
Db 752 -SLLMWTC-TVYAIKARGVPEFNEAKPIGFTWYTCIILWAFIPFEGTAQSAEKIYI 809
QY 663 KGLMLFGCFLAWETRNVSIP-ALNDSKYIGMSYVNGVICIIGAANSFLTRDQPNVQFC 721
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CLASSIFICATION	Functions by mediating intracellular signal transduction.
KEYWORDS	#superfamily metabotropic glutamate receptor 4 G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
FEATURE	
1-32	#domain signal sequence #status predicted #label SIG\
33-912	#product metabotropic glutamate receptor 4 #status predicted #label MEM\
588-610	#domain transmembrane #status predicted #label TRV\
625-645	#domain transmembrane #status predicted #label TIV\
657-675	#domain transmembrane #status predicted #label TII\
700-720	#domain transmembrane #status predicted #label TIV\
751-772	#domain transmembrane #status predicted #label TRV\
786-807	#domain transmembrane #status predicted #label TIV\
822-847	#domain transmembrane #status predicted #label TIV\
98,301,454,484,	
569	#binding-site carbohydrate (Asn) (covalent) #status predicted\
621,689,695,859,	
870	#binding-site phosphate (Ser) (covalent) #status predicted
SUMMARY	#length 912 #molecular-weight 101818 #checksum 808
Query Match	3.3%; Score 225; DB 2; Length 912;
Best Local Similarity	22.6%; Pred. No. 5,49e-15;
Matches	65; Conservative 93; Mismatches 101; Indels 29; Gaps 23;
Db	588 AVLPLEFLAVVG--IAATLFVYVYFVRNDYPIVAKSGNELSVLLAGLFCYATFFL--M- 643
Oy	482 SILSL-LTILQIMASALFEPN--TKNRKQKLIKSSPYMNNLLIGMLSYASLFEGLD 539
Db	644 ---IAEPDLGT--CSLRRIFELGSGISYVALLTKRNIYRFEQGRKSVSAPRISPASQ 639
Oy	540 GSFSSEKFEHLCTVRWILVGVTTAFGAFATRWVHALFKVVK--MKK-KIKNQKL 596
Db	700 LAIT--FLISLQILGICWFVDPDSHSVD--FODQRTLDP--FA-RGVAK-CDISDLSL 753
Oy	597 LVIWGGMLLIDLCIL-IC-WQAVDPLRRTVERYSMEPDPRGRDISIRPLLEHCENTHMTI 654
Db	754 -ICLL-GYSMLLV--TC-TYVAITRQVPEFFENAKRIGTMTYTTCVWLAFIPFEGTS 809
Oy	655 WLGIYVARKGLMFGCELANETNVSPI-ALNDSKRIKGSYVNWGIMCITGAASFLTR 713
Db	810 QSADKLVIQTTTLTVSVLSASVSLGMLYMPKVIYIIFFHEPQNPFRK 857
Oy	714 DQPNVQFC-IYALVI-I-FGSTITLCLVFPVKLITLTNPDAATQNRK 758
RESULT	6
ENTRY	A49874 #type complete
TITLE	metabotropic glutamate receptor 7 - rat
ALTERNATE_NAMES	metabotropic glutamate receptor mGluR7
ORGANISM	Formal name Rattus norvegicus #common.name Norway rat
DATE	02-Jul-1996 #sequence_revision 02-Jul-1996 #text.change 24-Sep-1999
ACCESSIONS	A49874; I57954
REFERENCE	A49874
Authors	Okamoto, N.; Hori, S.; Akazawa, C.; Hayashi, Y.; Shigemoto, R.; Mizuno, N.; Nakanishi, S.
#journal	J. Biol. Chem. (1994) 269:1231-1236
#title	Molecular characterization of a new metabotropic glutamate receptor mGluR7 couple to inhibitory cyclic AMP signal transduction.
#cross-references	MIMD:94117433
#status	A49874
#molecule_type	preliminary; translated from GB/EMBL/DBDUB
#residues	1-915 #label RES
#cross-references	GB:DI6817; NID:g458728; PIDN:BA04092.1; PID:g4587293
REFERENCE	I57954
Authors	Saugstad, J.A.; Kinzie, J.M.; Mulvihill, E.R.; Segerson, T.P.; Westbrook, G.L.
#journal	Mol. Pharmacol. (1994) 45:367-372

[illegible]

Qy	153	LSFATTPVLADKKKKYFFPFTVSDNAVNPAILKLKLKHKRRWRVGLTDQVQRFSSVRN	212
Db	180	PFLFDALQDYEVKRSVYIPPEAIDDEICKELKLMERQARVYVVMESSLARVFOIARDI	239
Qy	213	D-LGVLYGDED--ISDTESFSNDPCTSVKIKLKGNDVRRIILGQFDONMAKAFVCCAFEE	269
Db	240	GMEEGYVLM 250	
Qy	270	SMGSKTOWIT 280	
RESULT	8		
ENTRY		A42916 #type complete	
TITLE		metabotropic glutamate receptor mglur5 - rat	
ORGANISM		Formal_name Rattus norvegicus #common_name Norway rat	
DATE		04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 29-Jan-1999	
ACCESSIONS		A42916	
REFERENCE		A42916	
#authors		Abe,T.; Sugihara, H.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakaniishi, S.	
#journal		J. Biol. Chem. (1992) 267:13361-13368	
#title		Molecular characterization of a novel metabotropic glutamate receptor mglur5 coupled to inositol phosphate/Ca2+ signal transduction.	
#cross-references		MUTID:92317054	
#accession		A42916	
##status		preliminary	
##molecule_type		mRNA	
##residues		1-1171 ##label ABE	
##cross-references		GB:D10891; NID:g220813; PID:d1002186; PID:g220814	
##experimental_source		brain	
##note		sequence extracted from NCBI backbone (NCBIN:107749, NCBIP:107750)	
KEYWORDS		G protein-coupled receptor; transmembrane protein	
SUMMARY		#length 1171 #molecular_weight 128289 #checksum 8594	
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Best Local Similarity		28.3%; Pred. No. 1,66e-13;	
Matches		54; Conservative 57; Mismatches 61; Indels 19; Gaps 17;:	
Db	655	AMSYSAVTKNRNRIARILAGSK-KKICTKKPRFMSAQA-QLVIAF-LLTC---IG-IGII 707	
Qy	564	TTATGAFAKWRHAHAFKNVKKKKIKIKQKLLIVYGMLLLDLCITLQWADVPLRRT 623	
Db	708	VALFMEPPDIDMDHPSEIREYLLICNTNTDGV-VTP-L-GYNGLLIT-SCFYAFKTRNPV 764	
Qy	624	VERYSMEPDAGRII-SIRPLRECEHTHTMTIMGLIYAKGLMLFGC-FLAWEIRNVS 661	
Db	765	-ANFNKAQYIAFTWYTCIIMLAFVPI-YFGSNNYKIITMCF-S-VSL-SATVALGCM-FV 818	
Qy	682	IPALNDSKTYIGMSYVNGVICIIGAASFLRDPQVFCIVALVIFCSTITL-CLFEV 740	
Db	819	PKYVYIIIAKPE 829	
Qy	741	PKLITLRTNPD 751	
RESULT	9		
ENTRY		JC2132	
TITLE		#type complete	
ORGANISM		metabotropic glutamate receptor 5 A - human	
DATE		Formal_name Homo sapiens #common_name man	
ACCESSIONS		28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Jan-1996	
REFERENCE		JC2132	
#authors		JC2131	
#journal		Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.	
#title		Molecular cloning, Res. Commun. (1994) 199:1136-1143	
		Biochem. Biophys. Res. Commun. (1994) 199:1136-1143	
		isoforms of human metabotropic glutamate receptor subtype 5.	
#cross-references		MUTID:94197696	





```

DT
XX
DE
XX
Sequence 6, Application US/08486270
CC
XX
Sequence 6, Application US/08486270
CC
Patent No. 5807689
CC
GENERAL INFORMATION:
CC
APPLICANT: Daggett, Lorrie
CC
APPLICANT: Ellis, Steven B.
CC
APPLICANT: Liaw, Chen
CC
APPLICANT: Pontsler, Aaron
CC
APPLICANT: Johnson, Edwin C.
CC
APPLICANT: Hess, Stephen D.
CC
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,
CC
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF
CC
NUMBER OF SEQUENCES: 13
CC
CORRESPONDENCE ADDRESS:
CC
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
CC
STREET: 444 South Flower Street, Suite 2000
CC
CITY: Los Angeles
CC
STATE: CA
CC
COUNTRY: USA
CC
ZIP: 90071
CC
COMPUTER READABLE FORM:
CC
MEDIUM TYPE: Floppy disk
CC
COMPUTER: IBM PC compatible
CC
OPERATING SYSTEM: PC-DOS/MS-DOS
CC
SOFTWARE: PatentIn Release #1.0, Version #1.25
CC
CURRENT APPLICATION DATA:
CC
APPLICATION NUMBER: US/08/486,270
CC
FILING DATE: 02-JUN-1994
CC
CLASSIFICATION: 435
CC
PRIOR APPLICATION DATA:
CC
APPLICATION NUMBER: US 08/072,574
CC
FILING DATE: 04-JUN-1993
CC
ATTORNEY/AGENT INFORMATION:
CC
NAME: Reiter, Stephen E.
CC
REGISTRATION NUMBER: 31,192
CC
REFERENCE/DOCKET NUMBER: FP41 9772
CC
TELECOMMUNICATION INFORMATION:
CC
TELEPHONE: 619-546-4737
CC
TELEFAX: 619-546-9392
CC
INFORMATION FOR SEQ ID NO: 6:
CC
SEQUENCE CHARACTERISTICS:
CC
LENGTH: 879 amino acids
CC
TYPE: amino acid
CC
TOPOLOGY: linear
CC
MOLECULE TYPE: protein
CC
SEQUENCE 879 AA; 98878 MW; 4241110 CN;
SQ
Query Match 2.8%; Score 187; DB 1; Length 879;
Best Local Similarity 34.6%; Pred. No. 8,856-05;
Matches 28; Conservative 26; Mismatches 26; Indels 1; Gaps 1;
Db 145 VIGSGYSVSIVQVANLRLFIQIPISTASTAKLSRSDYFARTVPPDFYQAKMAEI 204
Oy 87 VEGVCPEVTSIIAESIQGMNLVQLSEFATTPVLADKKKYPFFRTVPSDNVAVPAIILKL 146
Db 205 LRFNMITYSTVASBGD-YGE 224
Oy 147 LKHYQWKRRVGTLDVQRFSE 167

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Search completed: Wed Mar 15 21:45:33 2000  
Job time : 34 secs.





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QY 150 YQMRKVGTLTODVQRFSEVRNDLTGVLYGEDIEISDSEFSNDPCTSVKKLKNDVRIIL 209
Db 196 GLFETEARKEVCEYKRELFPGKKYWFLLIGWYADNMF-KIY-DP-SINCTVDEMTAVE 252
QY 210 GQFDONNAARVFCACAEENNYGSKYQWIIIPGWYEPSMEQVHTEANSSRCIRKMLLAAME 269
Db 253 GHITTEIVMLNPANTRSISNMTSOEFVEKLTFRKLRHPEETGFOEAPLAYDAIMLALA 312
QY 270 GYGVDEPILSSKQIKTISGKTPOQY-EREYNN-KRSGVPSKFH-G-YAIDGIWIAKT 325
Db 313 LNKISGG--GGRSGVRLEDEYNNOITTDQIYRAMNSSFEQVSGHYVFDASGRMAATL 370
QY 326 LQRMETLHASSRHQRIDOFNYTDHTLGRILLNMMENEFNGVGYQVFF-RNGERMGITK 384
Db 371 IEQOGSGYKRIGYDSTKQDLMSW-SKTDKWIGSPPADQTLVTKTFRLSQKFIISVY 429
QY 385 FTQQRDSREKVEYEVNADVLTLEINDTIRQSGSEPRDKITIIIEQLRKISLPLXSILSA 444
Db 430 LSSIGIYLAVVCISFNINSHVRYIONSQPNLNLTAVGCSLAAVFPGLDGYHIGRN 489
QY 445 LTIIGMIMASAFLEFNNKRNQKLIKSSPYMNNLIILGMLSYASIFLFGDGSFYSEK 504
Db 490 QEPFVQCARLMLLGLGSLGSGMFTKIWMVHTVFTKKEKEMRKLTLEPKKIATVGL 549
QY 505 TFEFLCTVRWILTVGYTTAFGAMFAKTWRVHAIF--KNVKMK-KKIIKQKLLVIYGM 561
Db 550 VGMQVTLTAIWQIYDPLHRTIETFAKEPEKEDIVSILPOLEHSSRKMTWLGIFYGK 609
QY 562 LILDCLILICQAVDPLRKYREKISMEPDPAGRIDISIRPLEHEENHMTIWLIVYAYK 621
Db 610 GLLLILGIFLAYEFTKSVSTEKINDHRAVGMAIYNVAVLICITAPVMIILSSQODAAFAFA 669
QY 622 GLMLFECFLAMETRNVSIPALNDSKTYIGMSYVNGVICITGAIVSFLTRDQPNVQCIY 681
Db 670 SLAIVSSYITLVLVFVKMRRLITRGE 697
QY 682 ALVLIIFCSTITLCLVFPVKLITLTNP 709

RESULT 2
ID W40119 standard; Protein; 844 AA.
AC W40119;
DT 03-JUN-1998 (first entry)
DE Human GABA-BR1b receptor protein.
KW Gamma-aminobutyric acid; GABA-BR1a/B receptor; human; brain; agonist;
KW inhibitory neurotransmitter; peripheral nervous system; antagonist;
KW treatment; dementia; depression; anxiety; bronchial inflammation; asthma;
KW epilepsy; cognitive function.
OS Homo sapiens.
PN MO9746675-A1.
PD 11-DEC-1997.
PF 19-MAR-1997; E01370.
PR 22-NOV-1996; US-756091.
PR 30-MAY-1996; US-655716.
PA (NOVS ) NOVARTIS AG.
PI Bettler B, Bittiger H, Froestl W, Kaupmann K, Mickel SJ;
DR N-PSDB: V10267.
PT Purified GABA-B receptor or receptor protein - and antagonists of
PT these which may be useful in treating nervous system disorders
PS Claim 4; Page 86-90; 108pp; English.
CC This sequence represents a novel human GABA-B receptor protein,
CC GABA-BR1b. GABA (gamma-aminobutyric acid) is the major inhibitory
CC neurotransmitter found in the brain and peripheral nervous system
CC and this receptor may be used for the identification of GABA-B
CC receptor agonists and antagonists. Such proteins may be used in
CC treatment of dementia, depression, anxiety, epilepsy, spasticity,
CC bronchial inflammation or asthma or to improve cognitive function.
CC GABA-B receptor ligands and probes derived from this sequence can be
CC used to assay for GABA-B receptors or DNA encoding them.
SQ Sequence 844 AA;
```

Query Match

25.7%; Score 1687; DB 1; Length 844;

Best Local Similarity 36.2%; Pred. No. 1,04e-131;  
Matches 249; Conservative 180; Mismatches 243; Indels 16; Gaps 14;

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Db 68 GQACQPAVENALDEDVNSRDILDPYELKLIHNSKCDPGQATYLYELLYNDPIKITIIMP 127
QY 31 GRGLPAVEALIDEQIRNE-SILRPFLDLRLTYDECDNAGLAKAFYDAIKYGRPHLAVFG 89
Db 128 G-CSSVTLVAEAAARMNLIIVLSGSSSPALSNORPPEFRHPSTLNPFRVTKFEK 186
QY 90 GVCPSVTSLAESLQGNLVLSFAATTPVLADKKTPIYFKTVPSONAVNPALKLKH 149
Db 187 WGMKRIATIQOTTEVFSTLDDLEERYKEAGIEITFRQSFSPDPAVYKMLKRODAIIV 246
QY 150 YQMRKVGTLTODVQRFSEVRNDLTGVLYGEDIEISDSEFSNDPCTSVKKLKNDVRIIL 209
Db 247 GLFETEARKEVCEYKRELFPGKKYWFLLIGWYADNMF-KIY-DP-SINCTVDEMTAVE 303
QY 210 GQFDONNAARVFCACAEENNYGSKYQWIIIPGWYEPSMEQVHTEANSSRCIRKMLLAAME 269
Db 304 GHITTEIVMLNPANTRSISNMTSOEFVEKLTFRKLRHPEETGFOEAPLAYDAIMLALA 363
QY 270 GYGVDEPILSSKQIKTISGKTPOQY-EREYNN-KRSGVPSKFH-G-YAIDGIWIAKT 325
Db 364 LNKISGG--GGRSGVRLEDEYNNOITTDQIYRAMNSSFEQVSGHYVFDASGRMAATL 421
QY 326 LQRMETLHASSRHQRIDOFNYTDHTLGRILLNMMENEFNGVGYQVFF-RNGERMGITK 384
Db 422 IEQOGSGYKRIGYDSTKQDLMSW-SKTDKWIGSPPADQTLVTKTFRLSQKFIISVY 480
QY 385 FTQQRDSREKVEYEVNADVLTLEINDTIRQSGSEPRDKITIIIEQLRKISLPLXSILSA 444
Db 481 LSSIGIYLAVVCISFNINSHVRYIONSQPNLNLTAVGCSLAAVFPGLDGYHIGRN 540
QY 445 LTIIGMIMASAFLEFNNKRNQKLIKSSPYMNNLIILGMLSYASIFLFGDGSFYSEK 504
Db 541 QEPFVQCARLMLLGLGSLGSGMFTKIWMVHTVFTKKEKEMRKLTLEPKKIATVGL 600
QY 505 TFEFLCTVRWILTVGYTTAFGAMFAKTWRVHAIF--KNVKMK-KKIIKQKLLVIYGM 561
Db 601 VGMQVTLTAIWQIYDPLHRTIETFAKEPEKEDIVSILPOLEHSSRKMTWLGIFYGK 660
QY 562 LILDCLILICQAVDPLRKYREKISMEPDPAGRIDISIRPLEHEENHMTIWLIVYAYK 621
Db 661 GLLLILGIFLAYEFTKSVSTEKINDHRAVGMAIYNVAVLICITAPVMIILSSQODAAFAFA 720
QY 622 GLMLFECFLAMETRNVSIPALNDSKTYIGMSYVNGVICITGAIVSFLTRDQPNVQCIY 681
Db 721 SLAIVSSYITLVLVFVKMRRLITRGE 748
QY 682 ALVLIIFCSTITLCLVFPVKLITLTNP 709

RESULT 3
ID W40118 standard; Protein; 844 AA.
AC W40118;
DT 03-JUN-1998 (first entry)
DE Rat GABA-BR1b receptor protein.
KW Gamma-aminobutyric acid; GABA-BR1b receptor; rat; brain; agonist;
KW inhibitory neurotransmitter; peripheral nervous system; antagonist;
KW treatment; dementia; depression; anxiety; bronchial inflammation; asthma;
KW epilepsy; cognitive function.
OS Rattus norvegicus.
PN MO9746675-A1.
PD 11-DEC-1997.
PF 19-MAR-1997; E01370.
PR 22-NOV-1996; US-756091.
PR 30-MAY-1996; US-655716.
PA (NOVS ) NOVARTIS AG.
PI Bettler B, Bittiger H, Froestl W, Kaupmann K, Mickel SJ;
DR N-PSDB: V10266.
PT Purified GABA-B receptor or receptor protein - and antagonists of
PT these which may be useful in treating nervous system disorders
```







PT New isolated human metabotropic glutamate receptors - used for  
PT detection, diagnosis and therapy of diseases associated with the  
PT receptors, eg. stroke, epilepsy and Alzheimer's disease.  
PS Claim 2: Page 40-43; 55pp; English.  
PC mRNA from the human cerebellum was used to construct a cDNA  
CC library. cDNA was amplified by PCR primers (T03896-97) based on rat  
CC mGluR4 sequences and with the primers given in T03898-99 to obtain  
CC cDNA encoding human mGluR4.  
CO Sequence 912 AA;

Query Match	3.58;	Score 238;	DB 1;	Length 912;
Best Local Similarity	21.68;	Pred. No. 1.09e-07;		
Best Match	62;	Conservative	98;	Mismatches 100;
			Indels	27;
			Gaps	22;

```

Db      588  AULPLFLAAVVG-IAALFVVTFRYNDPTFVSAAGSELVSLAALFICATFTEL-M- 643
Oy      440  SILBA-LTIIGMIAVSAFLFFN-IRKNNOQLIKMSSSYMMNNLLILGMLSYAIFLFGID 497
Db      644  --IAEPDLGT-CSLRRIETGLGMSISYAALLTKNRITFIEQGRSVSAPEFISPAO 699
Oy      498  GSPFSEKFEETLCVTRMTILVGTTFATFAGMAFKAFTVAHAFENVR-K-MK-DIIDOKU 554
Db      700  LAIFFSLSIOL-LGICWMPFVVDSSHVVO-FODORFLDPR-EA-RGVLK-CDISDLSL- 753
Oy      555  LVIYGGMLIDLCILIC-MQAVNIDRLRTVEKYSMEPPDPAORDISIRPLEHCENHTIWI 613
Db      754  ICLL-GYSMLLV-TC-TVAIAIKTRGVPEFFENEAKPFGFMITTCIYWLAFIIFGTSQ 810
Oy      614  LGIYAVAYKGLMLMEGCEFLAMETRVNSIP-ALNDSKYIGMSVYVNGVICILGAAVSEFLTRD 672
Db      811  SADRKUYIOTTLTVSVSLASASVSLGMYLMPVYVYLIFHEPEONVPPKRK 857
Oy      673  QPNVOCF-IVALVIT-I-FCSTIITCLVIVFPRKILIRLNRPDAQTGNRR 726

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RESULT 9
ID R72092 standard; Protein; 912 AA.
AC R72092:
DT 26-SEP-1995 (first entry)
DE Human mGluR4.
KW Human metabotropic glutamate receptor subtype 4; mGluR4; hmGluR4;
   signal transducer.
OS Homo sapiens.
PN WO9508627-A.
PS 30-MAR-1995.
PF 07-SEP-1994; E02991.
PR 20-SEP-1993; EP-810663.
PI 19-AUG-1994; GB-016553.
PA (CIBA) CIBA GEIGY AG.
PI Flor PJ, Kneofel T, Kuhn R, Lindauer K, Puettner I;
DR MPI; 95-139596/18.
DR N-PSDB: 089342.
PT Human metabotropic glutamate receptor sub-type(s), esp. 4, 6 and
PT 7 also corresp. DNA and antibodies, useful for identifying
PT cpds. which modulate signal transduction activity
PS Claim 2; Page 44:48; 110pp; English.
CC Human metabotropic glutamate receptor subtype 4 (hmGluR4) cDNA
CC Human metabotropic glutamate receptor subtype 4 (hmGluR4) cDNA
CC clones were isolated from a cerebellum cDNA library using a rat
CC mGluR4 probe. Clone cmr20 lacked the 5' end of the hmGluR4 gene.
CC PCR using human genomic or brain cDNA as template was used to
CC obtain a complete gene sequence (given in Q89342) encoding hmGluR4
CC (R72092). Recombinant hmGluR4 was produced in mammalian cells.
SQ Sequence 912 AA;

Query Match 3.5%; Score 228; DB 1; Length 912;
Best Local Similarity 21.6%; Pred. No. 1,09e-07;
Matches 62; Conservative 98; Mismatches 100; Indels 27; Gaps 22;

DB 588 AVUPLFLAVVG-IAALFVITFVRYNDPTPKASGRSLVLLAGIFLCATFEL--M- 643
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 440 SLISA-LTIIIGMIMASAFLEFN-INNRKOLTKMSSPYMNNDIILGGMILASLAFLEGLD 497
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

DB 644 ---IAEDDGT-CSLRIRIFLGMSISYALITKTRIRYRIFEOGRKRSVAPREISPAQ 699

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OY 498 GSFVSEKFEFLCYRWTLLVGGYTAFAFGAMFAKTWVHAIFKNVK--MKK-KIINDOKL 554
DB 700 LAIFSLISLQ-LGICWVFWDPSSHVD-FQDQRTLDR-PA-RGVLK-CDMSDLSL- 753
OY 555 LVIYVGMILLIDCLIC-WQAVDPLRRTVEKYSMEPPAPARDISIRPLEHCNTMTWTW 613
DB 754 ICLL-GYSMLLMV-TC-TVYAIKRGVPEFNEAKPIGFTWYTCIWLAFIDIFRQISQ 810
OY 614 LGIYVAYKGLMLFGCFLAMETRNVSIP-ALNDSKYIGMSVYVNGIMCIIIGAASVFLTRD 672
DB 811 SADKXIOTTLTVSVLSASVSLGMLYMPKVYIILFHPQONPKR 857
OY 673 QPNVQFC-IVALVI-I-FCSTITLCIVFVFKLITLRINPDAAQONRR 716

```

```

RESULT 10
ID W01099 standard; Protein: 877 AA.
AC W01099;
DT 03-JAN-1997 (first entry)
DE Metabotropic glutamate receptor subtype mglur6.
KM Metabotropic glutamate receptor; mglur6; neurological disease;
KW neurotransmitter.
OS Homo sapiens.
PN W09629404-A1.
PD 26-SEP-1996.
PF 18-MAR-1995; US-407875.
PR (SIBIR) SIBIR NEUROSCIENCES INC.
PI Daggett LP, Lu C;
DR WPI; 96-443180/44.
DR N-PSDB; T38322.
PT Human metabotropic glutamate receptor and related nucleic acid -
PT useful to identify related receptor subtypes and e.g. for drug
PT screening
PS Claim 2; Page 66-68; 79pp. English.
CC Novel human metabotropic glutamate receptor protein subtype mglur6
CC (W01099) participates in the G-protein-coupled response of cells to
CC glutamatergic ligands. Its amino acid sequence was determined from
CC cDNA clones (see also T38322) obt'd. from a human retinal cDNA library.
CC A splice variant has an alternative N-terminal sequence (see also
CC W01100). Recombinant receptors, practically free of contamination
CC by other receptors, can be produced in host cells. The receptors,
CC and cells expressing them, are used in drug screening to identify
CC cpts. that modulate mglur6.
SQ Sequence 877 AA;

```

```

Query Match 3.4%; Score 225; DB 1; Length 877;
Best Local Similarity 21.5%; Pred. No. 1,84e-07;
Matches 60; Conservative 91; Mismatches 106; Indels 22; Gaps 19;

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DB 592 LAVGIVATTVAATFVRYNNTPIYRASGRELSTVLLTGFLIYA-I-YF-L--MYAEP 645
OY 445 LTIIGMIMASAFLEFNINRNQKLIKMSPPYNNLIIIGMLSTASIFLFGDGSFVSEK 504
DB 646 G-AAVCAARBLFLGLTSLYSALLTKTNRIYRIFEQGRSVTPPPISPTSQLVTFSS 704
OY 505 TFEITCTYRTWILYGYTTAAGAMFAKTWRVHAIFKNVK--MKKK-IIRKQKLLIVYGM 561
DB 705 TSLQVYGAIANLWAGAPPSVID-YE-EQRTYDPEQA-RGVLK-CDMSDLSL-IGCL-GY- 757
OY 562 LLIDICILICQWAVDPLRRTVEKYSMEPPAPARDISIRPLEHCNTMTWTWIGIYAAK 621
DB 758 SLLMWTG-TVYAIKRGVPEFNEAKPIGFTWYTCIWLAFVPIFGTAQSAEKIYIQ 816
OY 622 GILMFGCFLAMETRNVSIP-ALNDSKYIGMSVYVNGIMCIIIGAASVFLTRDPNVQFC- 679
DB 817 TTTTLVSLSLASVSLGMLYPKYVILFHPQONPKR 855
OY 680 IVALVI-I-FCSTITLCIVFVFKLITLRINPDAAQONRR 716

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RESULT 11

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ID R72095 standard; Protein: 481 AA.
AC R72095;
DT 26-SEP-1995 (first entry)
DE Human mglur7 clone cmr5.
KW Human metabotropic glutamate receptor subtype 4; mglur7; hmglur7;
KW signal transducer.
OS Homo sapiens.
PN W09508627-A.
PD 30-MAR-1995.
PF 07-SEP-1994; E02991.
PR 20-SEP-1993; EP-810663.
PR 19-AUG-1994; GB-016553.
PA (CIBA) CIBA GEIGY AG.
PI Flor PJ, Knoepfel T, Kuhn R, Lindauer K, Puettner I;
DR WPI; 95-139596/18.
DR N-PSDB; Q89345.
PT Human metabotropic glutamate receptor sub-type(s), esp. 4, 6 and
PT 7 - also corresp. DNA and antibodies, useful for identifying
PT cpts. which modulate signal transduction activity
PS Claim 8; Page 69-72; 110pp. English.
CC Human metabotropic glutamate receptor subtype 7 (hmglur7) cDNA
CC clones were isolated from cDNA libraries using a rat mglur4 probe.
CC Fetal brain partial cDNA clone cmr5, encoding the protein given in
CC R72095, was obtained. The missing 5' region of the clone was
CC generated by PCR from brain cDNA. Sequence comparison of fetal
CC brain and hippocampus clones indicated the existence of 2 subtypes
CC of hmglur7 (R72097-98).
SQ Sequence 481 AA;

```

```

Query Match 3.3%; Score 214; DB 1; Length 481;
Best Local Similarity 22.9%; Pred. No. 1.25e-06;
Matches 65; Conservative 87; Mismatches 106; Indels 26; Gaps 22;

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```

DB 172 LAMGII-ATIFMAFIRYNDPIYRASGRELSTVLLTGFLCY--ITTF-L--MIA- 223
OY 445 LTIIGMIMASAFLEFN-INKRNQKLIKMSPPYNNLIIIGMLSTASIFLFGDGSFVSE 503
DB 224 KPDVAVCSFRRVFLGMCISYVALLTKTNRIYRIFEQGRSVTPARLISPTSQLATISS 283
OY 504 KTFETTLCTYRTWILYGYTTAAGAMFAKTWRVHAIFKNVK-K--KIIRKQKLLIVYGM 560
DB 284 LISVOLLGVRI-FEGVDPPRIID-YD-BHKYMNDEQA-RGVLK-CDTIDLOI-ICSL-G 336
OY 561 MLULDL-CLICQWAVDPLRRTVEKYSMEPPAPARDISIRPLEHCNTMTWTWIGIYIA 619
DB 337 YSILMAY-TC-TVYAIKRGVPEFNEAKPIGFTWYTCIWLAFPIFGTAQSAEKLY 394
OY 620 YKGLMFGCFLAMETRNVSIPA-LNDSKYIGMSVYVNGIMCIIIGAASVFLTRDPNVQF 678
DB 395 IQTTTLISNMLASVALGMLYMPKYIILFHPQONPKRSF 438
OY 679 C-IVALVI-I-FCSTITLCIVFVFKLITLRINPDAAQONRRQF 719

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```

RESULT 12
ID R72093 standard; Protein: 867 AA.
AC R72093;
DT 26-SEP-1995 (first entry)
DE Human mglur7 clone cmr2.
KW Human metabotropic glutamate receptor subtype 4; mglur7; hmglur7;
KW signal transducer.
OS Homo sapiens.
PN W09508627-A.
PD 30-MAR-1995.
PF 07-SEP-1994; E02991.
PR 20-SEP-1993; EP-810663.
PR 19-AUG-1994; GB-016553.
PA (CIBA) CIBA GEIGY AG.
PI Flor PJ, Knoepfel T, Kuhn R, Lindauer K, Puettner I;
DR WPI; 95-139596/18.
DR N-PSDB; Q89343.
PT Human metabotropic glutamate receptor sub-type(s), esp. 4, 6 and
PT 7 - also corresp. DNA and antibodies, useful for identifying

```

PT cpds, which modulate signal transduction activity  
PS Claim 6: Page 57-61; 110pp; English.  
CC Human metabotropic glutamate receptor subtype 7 (hmglur7) cDNA  
CC Clones were isolated from cDNA libraries using a rat mglur4 probe.  
CC Fetal brain partial cDNA clone cmr2, encoding the protein given in  
CC R72093, was obtained. The missing 5' region of the clone was  
CC generated by PCR from brain cDNA. Sequence comparison of fetal  
CC brain and hippocampus clones indicated the existence of 2 subtypes  
CC of hmglur7 (R72097-98).  
SQ Sequence 867 AA:  
  
Query Match 3.3%; Score 214; DB 1; Length 867;  
Best Local Similarity 22.9%; Pred. No. 1,25e-06;  
Matches 65; Conservative 87; Mismatches 106; Indels 26; Gaps 22;  
  
Db 542 LAMGII-ATIFWATFIRYNDPIVRSAGRELSVLTGIFLCY--ITTF-L---MIA- 593  
QY 445 LTIIGIMASAFLEFN-IKNRNOKLIKSSPYMNNLIILGMLSYASIFLFGDGSFVSE 503  
Db 594 KPDVAVCSFRVFLGCMCSYAAALLTKNRIKRIFEQGRKSVTAPRLISPTSLAITS 653  
QY 504 KTEETCTVTRWTLVGYTTAFGAMFAKTWRVHAIFKNVKR-K-KIKDQKLIYVGG 560  
Db 654 LISVOLLGVFI-MEGVDPNNIID-YD-EHKTNPDEA-RGVLK-CDITDLOI-ICSL-G 706  
QY 561 MLIDL-CILICQAVDPLRTRVEKYSMEPDPAGRDISTPPLHECENTHMTWLIYVA 619  
Db 707 YSILLMV-TC-TVAIKRGPENFENKAPIGFTMTTCIYWLAFIPFEGTAQSAEKLY 764  
QY 620 YKGLMFGCFIAMEFRNVSIPA-LNDSKYIGSVYNGVICIIGAASFLTRDQPNVQF 678  
Db 765 IOTTTLISNMLSASVALGMLYMPKVIITFIHPELVNQKRKRSF 808  
QY 679 C-IVALVI-I-FCSTITLCIVFVPRKLTILRTNPDAATONRRFOF 719  
  
RESULT 13  
ID R72097 standard; Protein; 915 AA.  
AC R72097;  
DE 26-SEP-1995 (first entry)  
DT Human mglur7a.  
KW Human metabotropic glutamate receptor subtype 4; mglur7; hmglur7;  
KW signal transducer.  
OS Homo sapiens.  
PN MO9508627-A.  
PD 30-MAR-1995.  
PE 07-SEP-1994; E02991.  
PR 20-SEP-1993; EP-810663.  
PR 19-AUG-1994; GB-016553.  
PA (CIBA ) CIBA GEIGY AG.  
PI Flor PJ, Knoepfel T, Kuhn R, Lindauer K, Puetner I;  
DR MPI; 95-139596/18.  
DR N-PSDB; Q89347.  
PT Human metabotropic glutamate receptor sub-type(s), esp. 4, 6 and  
PT 7 - also corresp. DNA and antibodies, useful for identifying  
PT cpds, which modulate signal transduction activity  
PS Claim 7: Page 82-87; 110pp; English.  
CC Human metabotropic glutamate receptor subtype 7 (hmglur7) cDNA  
CC clones were isolated from fetal brain and hippocampus cDNA libraries  
CC using a rat mglur4 probe, and the 5' region missing from these  
CC clones was generated by PCR from brain cDNA. Sequence comparison of  
CC fetal brain and hippocampus clones indicated the existence of 2  
CC subtypes of hmglur7, hmglur7a (given in R72097) and hmglur7b  
CC (R72098). Full-length cDNA clones (Q89347-48) encoding these  
CC proteins were expressed in mammalian cells.  
SQ Sequence 915 AA:  
  
Query Match 3.3%; Score 217; DB 1; Length 915;  
Best Local Similarity 22.9%; Pred. No. 7.41e-07;  
Matches 65; Conservative 87; Mismatches 106; Indels 26; Gaps 22;  
  
Db 597 LAMGII-ATIFWATFIRYNDPIVRSAGRELSVLTGIFLCY--ITTF-L---MIA- 648  
QY 445 LTIIGIMASAFLEFN-IKNRNOKLIKSSPYMNNLIILGMLSYASIFLFGDGSFVSE 503

QY 445 LTIIGIMASAFLEFN-IKNRNOKLIKSSPYMNNLIILGMLSYASIFLFGDGSFVSE 503  
Db 649 KPDVAVCSFRVFLGCMCSYAAALLTKNRIYRIFEQGRKSVTAPRLISPTSLAITS 708  
QY 504 KTEETCTVTRWTLVGYTTAFGAMFAKTWRVHAIFKNVKR-K-KIKDQKLIYVGG 560  
Db 709 LISVOLLGVFI-MEGVDPNNIID-YD-EHKTNPDEA-RGVLK-CDITDLOI-ICSL-G 761  
QY 561 MLIDL-CILICQAVDPLRTRVEKYSMEPDPAGRDISTPPLHECENTHMTWLIYVA 619  
Db 764 YSILLMV-TC-TVAIKRGPENFENKAPIGFTMTTCIYWLAFIPFEGTAQSAEKLY 819  
QY 620 YKGLMFGCFIAMEFRNVSIPA-LNDSKYIGSVYNGVICIIGAASFLTRDQPNVQF 678  
Db 820 IOTTTLISNMLSASVALGMLYMPKVIITFIHPELVNQKRKRSF 863  
QY 679 C-IVALVI-I-FCSTITLCIVFVPRKLTILRTNPDAATONRRFOF 719  
  
RESULT 14  
ID R80479 standard; Protein; 915 AA.  
AC R80479;  
DE 23-JAN-1996 (first entry)  
DT Rat metabotropic glutamate receptor mglur7.  
KW Metabotropic glutamate receptor; mglur7; cerebral ischaemia;  
KW migraine; Parkinson's disease; Huntington's chorea.  
OS Rattus rattus.  
FH Key  
FH peptide  
FT 1..32 Location/Qualifiers  
FT /note= "signal peptide"  
FT 591..613  
FT /note= "transmembrane domain-I"  
FT 628..648  
FT /note= "transmembrane domain-II"  
FT 660..678  
FT /note= "transmembrane domain-III"  
FT 703..723  
FT /note= "transmembrane domain-IV"  
FT 754..775  
FT /note= "transmembrane domain-V"  
FT 789..810  
FT /note= "transmembrane domain-VI"  
FT 826..850  
FT /note= "transmembrane domain-VII"  
PN MO9518154-A1.  
PD 06-JUL-1995.  
PE 29-DEC-1994; U14989.  
PR 30-DEC-1993; US-176401.  
PA (UTOR-) UNIV OREGON HEALTH SCI.  
PA (ZYMO ) ZYMOGENETICS INC.  
PI Kinzie MJ, Mulvihill ER, Saugstad JA, Segerson TP;  
PI Westbrook GL;  
DR MPI; 95-246338/32.  
DR N-PSDB; Q99209.  
PT New metabotropic glutamate receptor mglur7 and related antibodies  
PT useful for identifying its modulators, diagnosis and treatment of  
PT cerebral ischaemia etc.  
PS Claim 1: Page 25; 41pp; English.  
CC The mglur7 protein can bind glutamate and induce cytoplasmic  
CC signal transduction. It is especially involved in regulation of  
CC mitral/tufted neurons in the olfactory bulb and may act by  
CC mediating inhibition of transmitter release at particular  
CC glutamatergic synapses.  
SQ Sequence 915 AA:  
  
Query Match 3.3%; Score 214; DB 1; Length 915;  
Best Local Similarity 22.9%; Pred. No. 1,25e-06;  
Matches 65; Conservative 87; Mismatches 106; Indels 26; Gaps 22;  
  
Db 597 LAMGII-ATIFWATFIRYNDPIVRSAGRELSVLTGIFLCY--ITTF-L---MIA- 648  
QY 445 LTIIGIMASAFLEFN-IKNRNOKLIKSSPYMNNLIILGMLSYASIFLFGDGSFVSE 503



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: March 19, 2000, 17:26:20 ; Search time 2783.46 Seconds

(without alignments)  
-3079.517 Million cell updates/sec

Title: US-09-211-755-3  
Perfect score: 2823  
Sequence: 1 ATGGCTTCCCGCCGAGCTC.....TCATGCTCTGGGCTGTAG 2823  
Scoring table: IDENTITY\_NUC  
Searched: 821193 seqs, -1518192014 residues  
Database : GenEmbl:\*  
Word size : 0  
Number of hits that pass the threshold : 1642386

1: gb\_ba1:\*  
2: gb\_ba2:\*  
3: gb\_cm:\*  
4: gb\_ov:\*  
5: gb\_pat:\*  
6: gb\_ph:\*  
7: gb\_pl1:\*  
8: gb\_pl2:\*  
9: gb\_pr1:\*  
10: gb\_pr2:\*  
11: gb\_pr3:\*  
12: gb\_to:\*  
13: gb\_sts:\*  
14: gb\_sy:\*  
15: gb\_un:\*  
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17: em\_fun:\*  
18: em\_hum1:\*  
19: em\_hum2:\*  
20: em\_in:\*  
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26: em\_pl:\*  
27: em\_ro:\*  
28: em\_sts:\*  
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30: em\_un:\*  
31: em\_v1:\*  
32: gb\_htg1:\*  
33: gb\_htg2:\*  
34: gb\_in1:\*  
35: gb\_in2:\*  
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37: em\_ba2:\*  
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43: gb\_htg5:\*  
44: gb\_htg6:\*  
45: gb\_htg7:\*  
46: em\_htg1:\*  
47: em\_htg2:\*  
48: em\_htg3:\*  
49: em\_hum5:\*

50: gb\_pl3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query				ID	Description
	Score	Match	Length	DB		
1	2823	100.0	2823	12	AF074482	AF074482 Rattus no
2	2816.6	99.8	3288	12	AF109405	AF109405 Rattus no
3	2816.2	99.8	5459	12	AF058795	AF058795 Rattus no
4	2805.2	99.4	5614	12	RN0011318	AF011318 Rattus no
5	2348.2	83.2	5786	11	AF056085	AF056085 Homo sapi
6	2346.6	83.1	2826	10	AF056085	AF056085 Homo sapi
7	2346.6	83.1	2826	40	AF074483	AF074483 Homo sapi
8	2346.6	83.1	3240	40	AF095784	AF095784 Homo sapi
9	2345	83.1	3075	40	AF069755	AF069755 Homo sapi
10	2345	83.1	3155	40	AF099033	AF099033 Homo sapi
11	486.4	17.2	740	11	AF095724	AF095724 Homo sapi
12	415	14.7	743	11	AF095723	AF095723 Homo sapi
13	410.2	14.5	3989	35	AF145639	AF145639 Drosophila
14	347	12.3	2328	9	HSN225029	AJ225029 Homo sapi
15	347	12.3	2535	10	HSN225028	AJ225028 Homo sapi
16	346	12.3	4281	9	HSN225028	AJ225028 Homo sapi
17	346	12.3	4445	9	HSN225028	AJ225028 Homo sapi
18	346	12.3	2886	10	HSN225028	AJ225028 Homo sapi
19	346	12.3	2700	10	HSN225028	AJ225028 Homo sapi
20	346	12.3	3192	40	AF099148	AF099148 Homo sapi
21	342.4	12.1	3202	12	AB016161	AB016161 Rattus no
22	341.8	12.1	4220	9	HSN225028	AJ225028 Homo sapi
23	341.8	12.1	2535	12	RN0011318	AF011318 Rattus no
24	339.6	12.0	2883	12	RN0011318	AF011318 Rattus no
25	337	11.2	4365	12	AF114168	AF114168 Mus muscu
26	255	9.0	3000	12	AB016160	AB016160 Rattus no
27	175.4	6.2	153726	33	AC007800	AC007800 Homo sapi
28	168.4	6.0	153790	42	AC011957	AC011957 Homo sapi
29	146	5.2	465	9	AB015334	AB015334 Homo sapi
30	122.6	4.3	116154	33	AC008195	AC008195 Drosophila
31	122.6	4.3	30107	43	AC014407	AC014407 Drosophila
32	118.8	4.2	116154	33	AC008195	AC008195 Drosophila
33	110.6	3.9	153790	42	AC011957	AC011957 Homo sapi
34	95.4	3.4	37895	34	CE12K180	U58748 Caenorhabdi
35	93.4	3.3	79987	35	AC004420	AC004420 Drosophila
36	93.4	3.3	74795	45	AC018197	AC018197 Drosophila
37	74.8	2.6	79884	34	AC002502	AC002502 Drosophila
38	72.8	2.6	1546	11	AF075292	AF075292 Homo sapi
39	70.2	2.5	10147	12	RN0011318	AF011318 Rattus no
40	64.2	2.3	42030	40	AC007565	AC007565 Homo sapi
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#### ALIGNMENTS

RESULT 1  
AF074482 2823 bp mRNA 07-JAN-1999  
LOCUS Rattus norvegicus GABA-B receptor 2 (GABA-BR2) mRNA, complete cds.  
DEFINITION AF074482  
ACCESSION AF074482  
VERSION AF074482.1 GI:4107510  
KEYWORDS  
SOURCE Norway rat.  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;  
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
REFERENCE  
1 (bases 1 to 2823)





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Db 1261 AGATGGAGCACTTAATTAATTTCAATTTCAAGACAGAGAGAGGTGAAGGTCGGCGAA 1320
Qy 1321 TACAAGCGGTGGCTGACACACTGGAGATCATTAATGACACCTTAAGTTTCCAGGGGTCC 1380
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Qy 1381 GAGCAGCCCAAGAGCAAGACCATTCCTGGAGCAGTTGGAAGATCTCGTTCACAGT 1440
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Qy 1801 GGGGGCATGCTGCTCATGACCTTGATCTGATCTGTTGGCAGGCTGAGACCCCTG 1860
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Qy 1861 CGGAGGACAGTAGAGAGGTAAAGCATGAGCGGAGCCGAGGCGCGGACATCTCATC 1920
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Qy 1921 CGCCCATGCTGGAACACTGCGAAACACCCACATGACCATCTGGCTTGGCATGTCTAC 1980
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Qy 2461 AAGACACATACATCAAAAGAAATCACTACCAAGAGCTCAACGACATCTCAGCTTGGC 2520
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Qy 2821 TAG 2823
Db 2821 TAG 2823

RESULT 2
AF109405 3288 bp mRNA ROD 07-JAN-1999
LOCUS AF109405 3288 bp mRNA ROD 07-JAN-1999
DEFINITION Rattus norvegicus GABA-B receptor 2 mRNA, complete cds.
ACCESSION AF109405
VERSION AF109405.1 GI:4107514
KEYWORDS
SOURCE
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE
1 (bases 1 to 3288)
Kuner, R., Kohr, G., Grunewald, S., Eisenhardt, G., Bach, A. and
Kornau, H.-C.
Role of heteromer formation in GABAB receptor function
Science 283 (5398), 74-77 (1999)
MEDLINE
99102694
REFERENCE
2 (bases 1 to 3288)
Kuner, R., Koehr, G., Grunewald, S., Eisenhardt, G., Bach, A. and
Kornau, H.-C.
Direct Subunit
Submitted (25-NOV-1998) Department of Neuroscience, BASF-Lyxx
Bioscience AG, Im Neuenheimer Feld 515, Heidelberg D-69120, Germany
FEATURES
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APRPPSSPLSLIMGLMPLTEKVASGSIGRGLVPAVELAIQINIESILRPYFDLRL
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VLADKKIPIFFRIYPSDNANVAILKLKIFRRRVGTLVQDQRESEVANDLTGVL
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Db	1798	GTGGGGCTACCAACTCCCTTTTGGGGCCATGTTGGAAAAGACTGGAGGGTCCATGCCATC	1857
Qy	1741	TTGCAAAATGTGAAGATGGAAGAAGATCATCAAAAGCCGGAAGCGCTTGTGATTGTG	1800
Db	1858	TTCAAAATGTGAAGATGGAAGAAGATCATCAAAAGCCGGAAGCGCTTGTGATTGTG	1917
Qy	1801	GGGGGCACTGCTGCTCATGCACCTGTGCATCTGTATCTTTGGCAGGCTGTGGACCCCTG	1860
Db	1918	GGGGGCACTGCTGCTCATGCACCTGTGCATCTGTATCTTTGGCAGGCTGTGGACCCCTG	1977
Qy	1861	CGGAGGCACTAGAGAGTACAGCATGAGCGCGGAGCCGAGAGCGCGGAGCATCTCATC	1920
Db	1978	CGGAGGCACTAGAGAGTACAGCATGAGCGCGGAGCCGAGAGCGCGGAGCATCTCATC	2037
Qy	1921	CGGCCATTTGCTGAGACACTGCGAAAACACCCACATGACCATCTGGCTTGGCATTTGCTAC	1980
Db	2038	CGGCCATTTGCTGAGAACACTGCGAAAACACCCACATGACCATCTGGCTTGGCATTTGCTAC	2097
Qy	1981	GGCTACAAAGGGGGTCCCTCATGCTATTCGGTGTGTTTCTTGGCATGGGAAACCCGCAATGTG	2040
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Qy	2041	AGCATCCCTCCCTCAACGACAGCATGTCATCGGCATGAGTGTGTACATATGTGGGATC	2100
Db	2158	AGCATCCCTCCCTCAACGACAGCATGTCATCGGCATGAGTGTGTACATATGTGGGATC	2217
Qy	2101	ATGTGCATCATCGGGGCTGCTGTCTCTCTTCCTTCTGAGCGGTGACACCCCAAGTCAATTC	2160
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Qy	2221	CCAAAGCTCATTACTGTGAGGACAAACCTGACGCAACCCATCAGACAGCGGTTCCAG	2280
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Db	2518	ATTCACAGAGCTGGACAAAGACTTGGAAAGAGTACCATCTGACTACAAAGACACACAGAG	2577
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Qy	2521	AACTTACAGAGAGCACAGATGAGGAAAGGCCATTCTAAAAAATCACCTGCATCAAAAC	2580
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Qy	2641	ATCAACTCCCGGAGGACATCAACGCGCGCTGTGCTCCAGCTCCCATCTCTTCACAC	2700
Db	2758	ATCAACTCCCGGAGGACATCAACGCGCGCTGTGCTCCAGCTCCCATCTCTTCACAC	2817
Qy	2701	GGCTACCTCCCATCCATCGAGAGGGGTGGATGGCAAGCTGCTCAAGCGCTGTCAGGCT	2766
Db	2818	GGCTACCTCCCATCCATCGAGAGGGGTGGATGGCAAGCTGCTCAAGCGCTGTCAGGCT	2877
Qy	2761	ACCGGCAACCCCTCGCAAGACAGCATGTCACACCTCTCTCGAATCATGTGCTCGGGCTG	2820

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QY	2821	TAG	2823	
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LOCUS	AF058795	5459 bp	mRNA	ROD
DEFINITION	Rattus norvegicus GABA-B receptor gb2 mRNA,			15-OCT-1998
ACCESSION	AF058795			complete cds.
VERSION	AF058795.1	GI:3746525		
KEYWORDS	.			
SOURCE	Norway rat.			
ORGANISM	Rattus norvegicus			

REFERENCE 1 (bases 1 to 5459)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

AUTHORS	Clark, J.C., Lam, A. and Bonner
TITLE	gb2, A second GABA-B receptor

JOURNAL REFERENCE	Unpublished 2 (bases 1 to 5459)
1. J. C. ... and ...	...
2. J. C. ... and ...	...
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Submitted (09-APR-1998) Section on Genetics, NIMH, Bldg. 36, Rm. 10N101, Bethesda, MD 20892-1010

3D06, MSC 4094, Bethesda, MD 20892-4094, USA  
Location/Qualifiers

Source

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DEFINITION Rattus norvegicus mRNA for GABA-B R2 receptor.  
ACCESSION AV011318  
VERSION AV011318.1 GI:4029344  
KEYWORDS gaba-B R2 gene; GABA-B R2 receptor.  
SOURCE Norway rat.  
ORGANISM Rattus norvegicus  
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Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
REFERENCE 1 (bases 1 to 5614)  
AUTHORS Kaupmann, K.  
TITLE Direct Submission  
JOURNAL Submitted (17-SEP-1998) Kaupmann K., TA Nervous System, Novartis  
Pharma AG, K-125.6.20, CH-4002 Basel, SWITZERLAND  
2 (bases 1 to 5614)  
AUTHORS Kaupmann, K., Malitschek, B., Schuler, V., Heid, J., Frieestl, W.,  
Beck, P., Mosbacher, J., Bischoff, S., Kulik, A., Shigemoto, R.,  
Karschin, A. and Bettler, B.  
TITLE GABA(B)-receptor subtypes assemble into functional heteromeric  
complexes  
JOURNAL Nature 396 (6712), 683-687 (1998)  
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ACCESSION	AF056085		
VERSION	AF056085.1	GI:3719225	
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
AUTHORS	Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 5786)		
JOURNAL	Clark,J.C., Lam,A. and Bonner,T.I.		
REFERENCE	9b2, a second GABA-B receptor		
TITLE	Unpublished		
JOURNAL	2 (bases 1 to 5786)		
AUTHORS	Clark,J.C., Lam,A. and Bonner,T.I.		
TITLE	Direct Submission		
JOURNAL	Submitted (27-MAR-1998) Section on Genetics, NIMH, Bldg 36, Rm		
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[illegible]









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RESULT 7  
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DEFINITION Homo sapiens GABA-B receptor 2 mRNA, complete cds.  
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VERSION AF074483.1 GI:4107511  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
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REFERENCE 1 (bases 1 to 2826)  
AUTHORS Borowsky, B., Laz, T. and Gerald, C.  
TITLE Direct Submission  
JOURNAL Submitted (25-JUN-1998) Department of Molecular Biology, Synaptic  
Pharmaceutical Corporation, 215 College Road, Paramus, NY 07652,  
USA

REFERENCE 2 (bases 1 to 2826)  
AUTHORS Borowsky, B., Laz, T. and Gerald, C.  
TITLE Direct Submission  
JOURNAL Submitted (06-JAN-1999) Department of Molecular Biology, Synaptic  
Pharmaceutical Corporation, 215 College Road, Paramus, NY 07652,  
USA  
REMARK Sequence update by submitter  
COMMENT On Jan 7, 1999 this sequence version replaced gi:4038343.  
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BASE COUNT 696 a 840 c 721 g 569 t  
ORIGIN

Query Match 83.1%; Score 2346.6; DB 40; Length 2826;  
Best Local Similarity 89.7%; Pred. No. 0;



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ACCESSION	AF095784		
VERSION	AF095784.1	GI:4836217	
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SOURCE	human.		
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AUTHORS	1 (bases 1 to 3240) Liu, M., Parker, R., McCreia, K., Watson, J., Baker, E., Sutherland, G. and Herzog, H.		
TITLE	Cloning and characterization of a novel human GABA-B receptor subype with high affinity for GABA and low affinity for baclofen		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 3240)		
AUTHORS	Liu, M., Parker, R., McCreia, K., Watson, J., Baker, E., Sutherland, G. and Herzog, H.		
TITLE	Direct Submission		
JOURNAL	Submitted (15-NOV-1998) Neurobiology Program, Garvan Institute of Medical Research, 384 Victoria St., Sydney, NSW 2010, Australia		
FEATURES	Location/Qualifiers		

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REFERENCE Ng,G.Y.K., McDonald,T., Bonner,T., Rigby,M., Heavens,R.,  
AUTHORS Whiting,P., Chateaufort,A., Coulombe,N., Karguen,S., Caskey,T.,  
Evans,J., O'Neill,G.P. and Liu,Q.  
TITLE Cloning of a novel G-protein-coupled receptor GPR 51 resembling  
GABAB receptors expressed predominantly in nervous tissues and  
mapped proximal to the hereditary sensory neuropathy type 1 locus  
on chromosome 9  
JOURNAL Genomics 56 (3), 288-295 (1999)  
MEDLINE 9189236  
REFERENCE 2 (bases 1 to 3075)  
AUTHORS McDonald,T. and Liu,Q.  
TITLE Direct Submission  
JOURNAL Submitted (03-JUN-1998) Human Genetics, Merck Research Labs, West  
Point, PA 19486, USA  
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Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 3155)  
AUTHORS Martin,S.C., Russek,S.J. and Farb,D.H.  
TITLE Molecular identification of the human GABABR2: cell surface  
expression and coupling to adenylyl cyclase in the absence of  
GABABR1  
JOURNAL Mol. Cell. Neurosci. 13 (3), 180-191 (1999)  
MEDLINE 99263199  
REFERENCE 2 (bases 1 to 3155)











REFERENCE  
AUTHORS

1 (bases 1 to 3989)  
Rubin, G.M., Wan, K.H.,  
Harvey, D., Lewis, S.E.,  
Brokstein, P.,  
Barton, P.

## JOURNAL REFERENCE AUTHORS

Unpublished  
2 (bases 1 to 3989)  
Rubin C M, Khan K H, Harrow D, Lewis C E, Brock

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KEYWORDS	GABA-B receptor.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
AUTHORS	Primates; Catarrhini; Hominoidea; Homo.
JOURNAL	Kaupmann,K. Direct Submission Submitted (12-MAR-1998) Kaupmann K., TA Nervous System, Novartis Pharma AG, CH-125.6.20, CH-4002 Basel, SWITZERLAND 2 (bases 1 to 2928)
REFERENCES	Kaupmann,K., Schuler,V., Mosbacher,J., Bischoff,S., Bittiger,H., Heid,J., Froestl,W., Leonard,S., Pfaff,T., Karschin,A. and Beitler,B.: Human gamma-aminobutyric acid type B receptors are differentially expressed and regulate inwardly rectifying K+ channels Proc. Natl. Acad. Sci. U.S.A. 95 (25), 14991-14996 (1998) 99061981
TITLE	Location/Qualifiers
JOURNAL	1..2928
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 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;  
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 REFERENCE 1 (bases 1 to 2535)

**AUTHORS** White, J.H., Wise, A., Main, M.J., Green, A., Fraser, N.J., Disney, G.H., Barnes, A.A., Emson, P., Poord, S.M. and Marshall, F.H.  
**TITLE** Heterodimerization is required for the formation of a functional GABA(B) receptor  
**JOURNAL** Nature 396 (6712), 679-682 (1998)  
**REFERENCE** 99087321  
**MEDLINE** 2 (bases 1 to 2535)  
**AUTHORS** Fraser, N.J.  
**TITLE** Direct Substitution  
**JOURNAL** Submitted (16-OCT-1998) Fraser N.J., Receptor Systems, Cellular Sciences, GlaxoWellcome, Medicines Research Centre, Gunnels Wood Road, Stevenage, Herts, SG1 2NY, U.K.

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 QY 461 CTTTGCGCGCCACACAGCGCTGTGTTCTGCGATTAAGAAAGTACCCTATTTCTCCGGA 520  
 DB 446 CTTATGCTCCAGCTTACACAGCCCTGTCAACCGGAGCGTTTCCCCACTTCTTCCGGA 505  
 QY 521 CGTGTGCTGACAGACGCGGCTGAGCTGCTGATCCGGAAGCTCCGAGACCTTCCGCT 580  
 DB 506 CGACACCTATCGACACACTGACACACCTTACCCGCGTGAACCTTTGGAAGAGTGGGCT 565  
 QY 581 GCGGCGTGTGGGACACTGACGAGGAGCTGACGCGCTTCTCCAGGTGAGGATGACC 640  
 DB 566 GGAAGATGATGCTACATCCAGGAGACCACTGAGTCTTCACTTGAGACTTGAGAGC 625  
 QY 641 TGACTGGGCTTCTGATGAGGAGATTTGATGATCTTACAGACAGAGATTTCTCCATG 700  
 DB 626 TGGAGGACGAGTGAAGAGGCTGGAATTTGATGATTTTCCGCGAGATTTCTCTGAG 685  
 QY 701 ATCCCTGACACAGCGTCAAAAAGCTCAAGGGAATGACGTGCGGATCATCTTGCGCAGT 760  
 DB 686 ATCCAGCTGTGCGCGTCAAAAAGCTCAAGGGAATGACGTGCGGATCATCTTGCGCAGT 745  
 QY 761 TGACAGATATATGAGCAAGCAAAAGTCTGTGTGCTGCTGCGAGAGACATGTTGGCA 820  
 DB 746 TCTATGACACTGAAAGCCCGGAAGTTTTTTGTGAGTGTTCAAAGAGCTCTTTTGGGA 805  
 QY 821 GCAGTACCACTGATGATATCCCGGATGATGAGAGCGCTGCTGGGAGCAGTGCATG 880  
 DB 806 AGAATAGCTGTGCTTCTTATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 856  
 QY 881 TGGAGGCAATTCCTCCAGCTGCTGCTGCGAGAGCGCTGCTGCTGCTGCTGCTGCTGCT 940  
 DB 857 TCTTACAGCTTCTTATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 916  
 QY 941 TCGAGTGGACTTGTAGGCGCTGAGCTCAAGCAAAATCAAGACCATCTGAGGAGACCTC 1000  
 DB 917 TCACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 976  
 QY 1001 CACAGCACTATG-----AAGAGATGACAAAGCAAACTTGAAGCGTGGGCGCCAGCA 1054  
 DB 977 CCGAGAAATTTGTGAGAACTTACCAAGCGACTGAAAGAAACCTTGAGAGACAGGAG 1036  
 QY 1055 AGTTCATGAGTACGCTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1114  
 DB 1037 GCTTCAGAGAGCAACCGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1096  
 QY 1115 TGGAGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1174  
 DB 1097 AGACATCTGAGAGAGGCGCGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1156  
 QY 1175 ACACGCTGGGCAAAATCATCTTCAATGCAATGCAAGCAAGCAATCTTTCGGGCTACGG 1234  
 DB 1157 AGACCATTACGACCAAAATCTACCGGCGCAATGAATCTTGTGCTTGAAGGCTGTGCTG 1216  
 QY 1235 GTCAAGTGTGT---CCGGAAGGAGAGATGGAACCATTAATTTATCAATTTTC 1291  
 DB 1217 GCAATGT 1276  
 QY 1292 AAGACAGAGAGAGAGTGAAGTGGGCAATTAACAGCGGCTGGCTGACACACTGAGATGA 1351  
 DB 1277 AGGTGTGAGAGTGTGAGAGATTTGGCTATGATGACAGCAAGATGATGATGATGATGATGAT 1336  
 QY 1352 TGAATGACATTAAGTGTCCAGGGGTCCAGGACCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1411  
 DB 1337 CCAAAAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1393  
 QY 1412 AGCAGCTTGAAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1471  
 DB 1394 AGACATTCGCTTCTCTGTGACAGAAACTCTTTATCTGCTGCTGCTGCTGCTGCTGCTGCT 1453







GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: March 16, 2000, 17:40:53 ; Search time 151.92 Seconds

(without alignments)  
4649.106 Million cell updates/sec

Title: US-09-211-755-3

Perfect score: 2823  
Sequence: 1 ATGGCTTCCCCCGGAGCTC.....TCATGCTCTGGGCTGTAG 2823

Scoring table: IDENTITY\_NUC

Searched: 311585 seqs, 125096042 residues

Database: N\_Geneseq\_36.\*

Word size: 0

Number of hits that pass the threshold: 623170

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	347	12.3	2924	1	VI0267 Human GABA-BR1b re
2	346	12.3	2620	1	VI0265 Human GABA-BR1a/b
3	342.4	12.1	2837	1	VI0266 Rat GABA-BR1a rece
4	339.6	12.0	4376	1	VI0264 Rat GABA-BR1a rece
5	241.6	8.6	314	1	V88919 EST clone HM456. N
6	143.4	5.1	361	1	V81891 Human secreted pro
7	63.4	2.2	1028	1	Q27091 XY76 probe. DNA s
8	59.8	2.1	10596	1	VI01731 Plasmid pcISBON f
9	59.8	2.1	10596	1	TM0348 Vector plasmid pcm
10	59.8	2.1	9600	1	V21683 Nucleotide sequenc
11	59.8	2.1	799	1	V5851 Nucleotide sequenc
12	59.8	2.1	10596	1	VI0265 Human secreted pro
13	58.6	2.1	6407	1	T36035 rchd528 gene diffe
14	58.6	2.1	6407	1	V81825 Human rchd528 enco
15	58.6	2.1	6407	1	X26246 CDNA sequence of r
16	57.4	2.0	2974	1	O79630 Partial FRAXE reg
17	57	2.0	795	1	V55830 FLGA insert stabl
18	55	1.9	3109	1	O24962 DNA induced in hum
19	55	1.9	3132	1	V64276 Human BCR-1 CDNA.
20	54.8	1.9	11820	1	VI8130 Human chromosome 1
21	54.6	1.9	1089	1	N92576 Sequence of the 1.
22	54.6	1.9	1089	1	T93593 Elmeria tenella sp
23	53.4	1.9	5011	1	O65377 Multidrug resistanc
24	53.4	1.9	5011	1	T37173 CDNA encoding mult
25	53.4	1.9	4834	1	T14912 CDNA encoding mult
26	53.4	1.9	4864	1	T14911 CDNA encoding mult
27	53.4	1.9	4423	1	T14914 CDNA encoding mult
28	53.4	1.9	4885	1	T14910 CDNA encoding mult
29	53.4	1.9	4669	1	T14913 CDNA encoding mult
30	53.4	1.9	5011	1	V31497 Human multidrug re
31	53.4	1.9	5011	1	V31498 Human MDR variant
32	53.4	1.9	5011	1	X21977 Human MDR variant
33	53.4	1.9	5011	1	X21976 Human multidrug re
34	53.4	1.9	5011	1	X19817 Human multidrug re
35	53.4	1.9	5011	1	X19818 Human multidrug re
36	52.2	1.8	397	1	X51965 Human secreted pro
37	51.4	1.8	954	1	N90505 DNA encoding Group
38	51.4	1.8	957	1	V66836 Group B Elmeria te
39	51	1.8	678	1	V23145 5' fragment of Rat

## ALIGNMENTS

RESULT	ID	Score	Query Match	Length	DB ID	Description
1	VI0267	347	12.3	2924	1	VI0267 Human GABA-BR1b re
2	VI0265	346	12.3	2620	1	VI0265 Human GABA-BR1a/b
3	VI0266	342.4	12.1	2837	1	VI0266 Rat GABA-BR1a rece
4	VI0264	339.6	12.0	4376	1	VI0264 Rat GABA-BR1a rece
5	V88919	241.6	8.6	314	1	V88919 EST clone HM456. N
6	V81891	143.4	5.1	361	1	V81891 Human secreted pro
7	Q27091	63.4	2.2	1028	1	Q27091 XY76 probe. DNA s
8	VI01731	59.8	2.1	10596	1	VI01731 Plasmid pcISBON f
9	TM0348	59.8	2.1	10596	1	TM0348 Vector plasmid pcm
10	V21683	59.8	2.1	9600	1	V21683 Nucleotide sequenc
11	V5851	59.8	2.1	799	1	V5851 Nucleotide sequenc
12	VI0265	59.8	2.1	10596	1	VI0265 Human secreted pro
13	T36035	58.6	2.1	6407	1	T36035 rchd528 gene diffe
14	V81825	58.6	2.1	6407	1	V81825 Human rchd528 enco
15	X26246	58.6	2.1	6407	1	X26246 CDNA sequence of r
16	O79630	57.4	2.0	2974	1	O79630 Partial FRAXE reg
17	V55830	57	2.0	795	1	V55830 FLGA insert stabl
18	O24962	55	1.9	3109	1	O24962 DNA induced in hum
19	V64276	55	1.9	3132	1	V64276 Human BCR-1 CDNA.
20	VI8130	54.8	1.9	11820	1	VI8130 Human chromosome 1
21	N92576	54.6	1.9	1089	1	N92576 Sequence of the 1.
22	T93593	54.6	1.9	1089	1	T93593 Elmeria tenella sp
23	O65377	53.4	1.9	5011	1	O65377 Multidrug resistanc
24	T37173	53.4	1.9	5011	1	T37173 CDNA encoding mult
25	T14912	53.4	1.9	4834	1	T14912 CDNA encoding mult
26	T14911	53.4	1.9	4864	1	T14911 CDNA encoding mult
27	T14914	53.4	1.9	4423	1	T14914 CDNA encoding mult
28	T14910	53.4	1.9	4885	1	T14910 CDNA encoding mult
29	T14913	53.4	1.9	4669	1	T14913 CDNA encoding mult
30	V31497	53.4	1.9	5011	1	V31497 Human multidrug re
31	V31498	53.4	1.9	5011	1	V31498 Human MDR variant
32	X21977	53.4	1.9	5011	1	X21977 Human MDR variant
33	X21976	53.4	1.9	5011	1	X21976 Human multidrug re
34	X19817	53.4	1.9	5011	1	X19817 Human multidrug re
35	X19818	53.4	1.9	5011	1	X19818 Human multidrug re
36	X51965	52.2	1.8	397	1	X51965 Human secreted pro
37	N90505	51.4	1.8	954	1	N90505 DNA encoding Group
38	V66836	51.4	1.8	957	1	V66836 Group B Elmeria te
39	V23145	51	1.8	678	1	V23145 5' fragment of Rat

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QY 401 GTCCCTGTCATCTTATATATGCGGAGTCCCTCCAGAGCTGGAATCTGTGACGTTT 460
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 557 G---CTCTGTCTCCAGCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 613
QY 461 CTTTCGCCGCCACCGCCTGTTCTTGGGATGAAGAAGTACCCGATTTTCTTCCGGA 520
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 614 CTTATGGCTCCAGCTACACAGCCCTGTCAAAACCGGAGCGGTTCCCACTTCTTCCGGA 673
QY 521 CGGTCCTGAGACAGCGGCTGACCCCGCATCTGTAAGCTCCGAGAGCTTCCGCT 580
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 674 CGACCCCTACAGCCACTCCACACCCCTACCGCGTGAACCTCTTTGAAAAGTGGGCT 733
QY 581 GCGCGCTGTGGGACACATCCAGCAGACGTGACGCGCTTCTCCGAGTGAAGAAATGAC 640
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 734 GGAAGAAATGTTCTACCTACCTACGACACCACTAGGCTCTCACTTGACCTGAGACG 793
QY 641 TGACCTGGGCTTCTGATGAGGGAATGATGAGATCTCAGACAGAGAGTTTCTCCAAATG 700
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 794 TGGAGAAACGAGTGAAGAGGCTGGAAATGAGATTACTTTCGCCGAGATTCTTCTCAG 853
QY 701 ATCCCTGACACACGCTCAAAAAGCTCAAGGGAATGACGTGCGGATCTCTTGCCAGT 760
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 854 ATCCAGCTGTGCGGCTCAAAAACCTGAAGCGCCAGAGATGCCGAATCATCTGCGGACTTT 913
QY 761 TTGACCAAGATATGCGACAAAGTCTTCTGTGTGCTTCCGAGTGAAGAGATGTTGGCA 820
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Db 914 TCTATGAGACTGAAGCCCGGAAAGTTTGTGTGAGGTGTCAAGAGAGCTCTTCTTGGGA 973
QY 821 GCAGTACCAAGTGTATCTCCGGGATGTGACGAGCTGCTGTGGTGGGAGACAGTGCATG 880
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 974 AGAAATGAGCTGTGCTCTCATTTGGGTGTATGCTGACAAATTTGT-----TCMAA 1024
QY 881 TGGAGGCCAATTTCCCTCAAGCTGCTGCGCAGAAACCTCTGCGCTGATGGAAGTTACA 940
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1025 TCTATGAGACCTCTCTATCACTGACAGTGGATGAGATGAGTGGGAGGAGGAGCACA 1084
QY 941 TCGAGTGAAGTGTGAGCCCTGAGCTTCAAAACAATCAAGACCTCTCAGGAGAGATC 1000
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Db 1085 TCCACATGAGATGTGCTATGCTGATCTTGCAATACCCGACATTTCCCAACATCACT 1144
QY 1001 CACACAGATG-----AAAGAGATGACAAACAGACAGCTTCAAGGAGGAGGCCAGCA 1054
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1145 CCCAGAGATTTTGTGAGAACTAACAAGCAGACTGAAGAAACACCTGAGAGAGACAGAG 1204
QY 1055 AGTTCATGAGTACGCTTACGATGGGATCTGGTCAATGCCAAGACCTTACAGAGGCCA 1114
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Db 1205 GCTTCCAGAGAGCACCGCTGCGCTATGATGCCATCTGGGCTTGGCACTGGCCCTGACA 1264
QY 1115 TGGAGACACTGATGCTGAGTGAAGGACAGCGGATCCAGAGCTTCAATCAACAGACC 1174
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Db 1265 AGACATCTGAGAGAGGCGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 1324
QY 1175 ACACGCTGGGCAAAATCTCTCAATGCCATGAACGAGACCACTTCTTGGGGTCAAG 1234
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QY 1235 GTCAAGTTGTGT-----CCGGAACGGGAGAGATGGGACCAATTAATTAATCAATTC 1291
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY 1292 AAGACAGACAGAGTGAAGTGGCGGATACAAACGCGGTGGCTGACACAGTGAAGATCA 1351
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1445 AGGAGTGGAGCTTACAAAGAGATGGCTACTATGACAGACCAAGAGATCTTCTCTGTGT 1504
QY 1352 TCAATGACACCTAAGTGTCCAGGGGTCCGAGCACCAAGAGCAACACCATCTCTG 1411
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Db 1505 CCAAAACAGATTAATGATTTGAGAGGCTC-----CCCGAGCTGACAGACACCTGTATCA 1561
QY 1412 AGCAGCTTGAAGATCTGCTTCACTGTATAGACATCTGTGCTGCTGACACATCTCTG 1471
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1562 AGCAGATCTGCTTCTGTCACAGAAATCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTG 1621

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QY 1472 GCATGATCATGGCCAGCGCTTCTCTCTTCAACATCAAGAACCGGAACCAAAAGCTGA 1531
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Db 1622 GCATGTGCTACAGCTGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 1681
QY 1532 TTAAGATGCAAGCCCTTACATGAACACCTCATCTCTGGAGAGATGTCTCTAAG 1591
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1682 TCCAGATCTCAAGGCCCACTGAACCACTGACTGTGTGGGCTGTCTGAGCTGTGTG 1741
QY 1592 CATCCATCTCTCTTGTGGCTGATGGGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1651
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Db 1742 CTGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1801
QY 1652 TCTGACAGTCTGCGACCTGGAATTTCTACCGTGGGCTTACACAACTGCTTGTGGGCTATG 1711
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Db 1802 TCTGCGAGCGCCGCTCTGCGCTCTGCGCTCTGCGCTCTGCGCTCTGCGCTCTGCGCTCT 1861
QY 1712 TTGCAAAAGCTGTGAGGCTTCCATGCACTCTCA-----AAAAATGTAAGATGAAGA 1762
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Db 1862 TCACCAAGATTTGTGTGGGTTCACACAGGCTTTCACAAAGAAAGAAAGAAAGAGATGGA 1921
QY 1763 AGAAGATCATCAAGACCAAGACCTGCTGTGTGATTTGGGGGGGATGCTGTATGACC 1822
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Db 1922 GGAAGACTCTGGAACCTGGAAGCTGTATGCAAGAGGCTGCTGTGTGGGATGATG 1981
QY 1823 TGTGATCTCTGATCTGTGTGAGAGCTGTGAGACCCCTGCGAGAGACAGTGAAGAGTACA 1882
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1982 TCTCTACTCTGCGCATCTGCGAGATCTGTGAGACCTCTGACACGAGCATTTGAGACATTTG 2041
QY 1883 GCATGAGCCGAGACCCAGCAGGCGGAGACATCTCATCCGCCCCATTTGCTGTGAACATGGG 1942
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2042 CCAAGAGAGAACCTAAGAGAAATATGACGCTTATCTGTGCCCCAGCTGTGAACATTTG 2101
QY 1943 AAAACCCACATGACCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2002
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2102 GCTCCAGAGAAATGATATGATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2161
QY 2003 TATTCGTTGTTCTTGTGAGTGAAGAACCCGCAATGTGAGATCTCCCTGCCCCAAGACA 2062
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Db 2162 TGTGTGGAATCTTCTGCTGTATGAGCAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 2221
QY 2063 GCAGATGATGCGCATGATGATGTGTACAAATGTGGGATCATATGTGATCATGCGGCTGCTG 2122
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Db 2222 ACCGGCTGTGGGATGCGTATCTATCATATGTGCGAGTCTGTGCTGCTGCTGCTGCTGCTG 2281
QY 2123 TCTCTCTCTGACGGGTGACAGCCCAAGCTGCACTTGTGATGTGTGCTGCTGCTGCTGCTG 2182
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2282 TCACCATGATGTGTCCACGCGAGATGCAAGCTTGTGCTTGTGCTGCTGCTGCTGCTGCTG 2341
QY 2183 TCTTTCGACAGCAACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2242
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2342 TTTTCTCTCTATATCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2401
QY 2243 C 2243
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2402 C 2402
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RESULT 2
ID V10265
V10265 standard; cDNA to mRNA; 2620 BP.
AC V10265;
DT 03-JUN-1998 (first entry)
DE Human GABA-BR1a/b receptor cDNA.
KW Gamma-aminobutyric acid; GABA-BR1a/b receptor; human; brain; agonist;
KW inhibitory neurotransmitter; peripheral nervous system; antagonist;
KW treatment; dementia; depression; anxiety; bronchial inflammation; asthma;
KW epilepsy; cognitive function; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..2382
FT /tag= a
FT /product= GABA-br1a/b
FN MO9746675-A1.

```

PD 11-DEC-1997;  
PF 19-MAR-1997; E01370.  
PR 22-NOV-1996; US-756091.  
PR 30-MAY-1996; US-655716.  
PA (NOVS) NOVARTIS AG.  
PI Bettler B, Bittiger H, Froestl W, Kaupmann K, Mickel SJ:  
DR WPI: 98-042183/04.  
DR P-PSDB: W40117.  
PT Purified GABA-B receptor or receptor protein - and antagonists of  
PT these which may be useful in treating nervous system disorders  
PS Claim 3; Page 56-62; 108bp; English.  
CC This cDNA sequence encodes a novel human GABA-B receptor protein,  
CC GABA-BR1A/D. GABA (gamma-aminobutyric acid) is the major inhibitory  
CC neurotransmitter found in the brain and peripheral nervous system  
CC and this receptor may be used for the identification of GABA-B  
CC receptor agonists and antagonists. Such proteins may be used in  
CC treatment of dementia, depression, anxiety, epilepsy, spasticity,  
CC bronchial inflammation or asthma or to improve cognitive function.  
CC GABA-B receptor ligands and probes derived from this sequence can be  
CC used to assay for GABA-B receptors or DNA encoding them.  
SQ Sequence 2620 bp; 593 A; 716 C; 710 G; 601 T;

Query Match 12.3%; Score 346; DB 1; Length 2620;

Best local Similarity 50.6%; Pred. No. 8,6e-60;

Matches 1037; Conservative 0; Mismatches 975; Indels 36; Gaps 7;

QY 217 GGGGGGGGGCTGCTCCCCCGCTGGAGCTAGCCATGAGCA---GATCCGCAACGAGTCA 273  
DB 49 GGGCAGGCGCTGGCAGCGCGCGGTGGAGATGGCGCTGGAGGACGTGATAGCCAGGAGAC 108  
QY 274 CTCTGGCGCCCTACTCTCTGGACCTGCGACTATGACACCGAGTGAATGCAATGCAAG 333  
DB 109 ATCTGCGCGAGCTATGAGCTCAAGCTCATCCACGACAGCAAGTGTGATCCAGGCGCA 168  
QY 334 GGAATGAAGCCCTTCTATGAGCAATTAAGTATGAGCGCGCAATTTGATGTTTGA 393  
DB 169 GCCACCAAGTACATATGAGCTGCTTACAGACCCCTATCA--GATCATCTTTATG 225  
QY 394 GGGCTGTGCGTGTGTCACATCTATATGGCGAGTCCCTCCAGGCGGAATGCGTG 453  
DB 226 CTTGGTCGACGCTGTGCTCCACGCTGTGGCTGAGGCTCTGAGATGTGAAACCTCAT 285  
QY 454 CAGTTTCTTCGCGCGCACACGCTGTTCTTGGGATGAAGAAGTACCCGATTTTC 513  
DB 286 GTGCTTTCCTATGGCTCCAGTCCACGACCCCTGCAACCGGAGCGTTTCCCATCTTC 345  
QY 514 TTCCGAGCGTGGCTGACAGACGCGGTGAACCCCGCATCTGAAAGCTCTGAAACAC 573  
DB 346 TTCCGAAGCGCACCCATAGCCACACTCCACAAACCTACCCGCGTGAACCTTTTGAAG 405  
QY 574 TTCCGCGTGGCGGTGGGGGACACTCAGCAGGACGCGCTTCTCCGAGGTGAG 633  
DB 406 TGGGCTGTGAAGAAGATTGCTACCATCCAGCAGACATGAGTCTTACCTTCGACACTG 465  
QY 634 AATGACCTGACTGGGGTCTGTATGGGAGATATTTGATCTCAGACACAGAGATTTTC 693  
DB 466 GACGACCTGTGAAGACGATGAAAGAGGTGAATTTGATTTCTCCGCAAGTTTC 525  
QY 694 TCCATATATCCCTGACACAGGTCAAAAAGCTCAAGGGAATGACGTGGGATATGCTT 753  
DB 526 TTCTCAGATCCAGCTGTCCTCCGTCAAAACCTGAAGCGCCGAGATGCCGATCATGCTG 585  
QY 754 GCGCAGTTTGAAGATATGAGCAGCAAGCTCTTGTGCTTTCGAGAGAGCATG 813  
DB 586 GCACTTTTCTATGAGACGTGAAGCCGGAAGTTTGTGAGGTGTACAAAGAGGCTTC 645  
QY 814 TTGGCAGCAAGTACCATGATGATCATCCCGGATGCTACGACCTGCTGTGGAGAG 873  
DB 646 TTGGGAGAAAGTACGTGTGCTTCTCATTTGGGTGTGTGCTGACAAATGTCTCAAGA-- 704  
QY 874 GTGCAATGTGAAGCCAAATCTCAGCGTGCCTGGCAGAAAGCCTCTGGCTGCCATGAA 933

DB 704 -----TCTAGACCCCTTCTATCAACTGCACAGTGAATGATGACTAGCGCGGTGAG 756  
QY 934 GGTATATCGAGTGGACTTTGAGCCCTGAGGCTCCAAACAAATCAAGACATCTCAGG 993  
DB 757 GGGCATTATCAACTGATGATTTGATGCTGATATCTCGCAATACCGGACATTTCAAC 816  
QY 994 AAGATCCACAGCAGTATGAAGAAGATACACAGCAAAAGCTTCAG-----CGTGGG 1047  
DB 817 ATGATCCACAGCAATTTGTGAGAAATTAACCAAGCGATGAAAAAGACCCCTGAGAG 876  
QY 1048 CCCAGCAAGTTCCATGGGTACGGCTACGATGGGATCTGGGTCAATGCAAGACCTACAG 1107  
DB 877 ACAGAGCTTCCGAGGAGCAGCGCTGCTATGATGCCATCTGGGCTTGGGCTGAGGCC 936  
QY 1108 AGGCAATGAGACATCGATGCGATGACAGCAGCCAGCGGATCCAGACTTCAACTAC 1167  
DB 937 CTGAACAAGACATGTGAGAGGAGGCGCGCTTGTGTGGCGCTGAGGACTTCAACTAC 996  
QY 1168 ACAGACACAGCTGGGCAAAATATCTCTCAATGCCATGAAACGACCAACTTCTCGG 1227  
DB 997 AACAAACGACCATTTACCGACCAATCTACCGGCAATGAACCTTTGCTTTGAGGTT 1056  
QY 1228 GTCACGGGTCAAGTTGTGTT---CCGAGCGGGAGAGAAATGGGAACCATTAATTTACT 1284  
DB 1057 GTCTGTGGCATGTGTGTGTTGATGCCAGCGGCTCTGGATGGATGAGCGCTTATGAG 1116  
QY 1285 CAATTTCAAGACAGCAGAGAGTGAAGTGGCGAATACACGCGGTGCTGACACACTG 1344  
DB 1117 CAGCTTCAAGGTGGAGCTACAAAGATTGGTACTATGACACACCAAGATGATCTT 1176  
QY 1345 GAGATATCAATGACACCATTAAGTTCCAGGGTCCAGCCACCAAGCAAGCAATCATC 1404  
DB 1177 TCTGTGTCAAAACAGATTAATGATTGAGAGGTGCCCCCAGC---TGACCAACCTTG 1233  
QY 1405 ATTGTGAGCAGCTTCGGAAGATCTCGCTTCAGTATATGACATCTGTCGCTCAAC 1464  
DB 1234 GTATCAACAGATTTCCGCTTCTGTCACAGAAACCTTTATCTCGGTGATGCTCTGCC 1293  
QY 1465 ATCTCGGATGATGATGAGCAGCGCTCTCTCTTCAATCAATCAAGAACCGAACCA 1524  
DB 1294 AGCTGGGATGTGCTCTGATGTTGTGTGTCCTTAACTATCAATCTACATATGTC 1353  
QY 1525 AAGCTGATTAATATGATCAAGCCCTACATGAACCAACCTACATCTGGAGAGATGTC 1584  
DB 1354 CGTTATATCAAACTCAAGCCCAACCTGAACCACTGACCTGCTGTGCTGCTCACTG 1413  
QY 1585 TCTATGATCATCTCTCTCTTGGCTGATGGGTCTTCTGCTCAGAAAAGACCTTT 1644  
DB 1414 GCTTTAGCTGTGCTCTCTCCCTGGGGGTGATGTTACACATGTGGAGAACAGTTT 1473  
QY 1645 GAAACATCTGACAGGTCCGACCTGATGATCTCACCGTGGGTACACAACCTGCTTGG 1704  
DB 1474 CTTTGTGTGCGAGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1533  
QY 1705 GCGATTTTGAAGAAGCTGAGAGGCTCATGCGATCTTCAAAATGTGAAGTGAAGA- 1764  
DB 1534 TCCATGTTTCAACAAGATTGGTGGGTCCACAGGCTTTCACAAAGAAAGAAAGAA 1593  
QY 1764 -----GAGATCATCAAGAAGCAGAGCTGTGTGATTTGTGGGGGACATGCTGCTC 1815  
DB 1594 GAGTGGAGGAAGCTGTGAACCTGTGAAGCTGTATGACACAGTGGGCTGTGCTGGGC 1653  
QY 1816 ATGACCTGTGATCTGTGATCTGTGAGGCTGTGAGACCCCTGGGAGGACATGAG 1875  
DB 1654 ATGATGTCTCTCACTGTGCGATGTGCAATGTGAGACCTGTGACCGGACCATGAG 1713  
QY 1876 AGGTACAGATGAGCGCGAGCCAGCGGACGCGGACATCTCCATCCGCAATGCTGAA 1935  
DB 1714 ACATTTGCCAAGAGGAACCTTAAGAAATATTGAGCTGTATATCTGCCACGCTGAG 1773  
QY 1936 CACTGCAAAACACCAATGACATCTGCTTGGATTTGTGATGCTTACGCTTCAAGAGGCTC 1995  
DB 1774 CATTCAGCTCCAGGAAGATGATGCTGCTGAGCTTGTATGTTTACAAAGGGGCTG 1833

QY 1996 CTCATGCTATGCTGTTCTTGGCAGGGAACCCGCAATGTCAGCATCCCTCCCTC 2055  
DB 1834 CTGCTGCTGCTGGATCTTCTTCTTATGAGCAAGAGTGTCTGAGAGATG 1893  
QY 2056 AAGCAGACAGAGACATGCGCATGATGTCATGATGAGGAGATGATGATGAGG 2115  
DB 1894 AATGATACACCGGCTGTGGCATGGCTATCTCAATGTGGAGTCTGTGCTCATCT 1953  
QY 2116 GCTGCTGCTCTCTTCTGACGGGTGACAGCCCAAGTCGATTCGATGTCGCTG 2175  
DB 1954 GCTGCTGCTACCATGATGTCCTGTCAGACCCAGATGACGCTTGGCTTGGCTCT 2013  
QY 2176 GTCATGCTGCTGACGACCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2235  
DB 2014 GCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2073  
QY 2236 CTGAGGAC 2243  
DB 2074 CTGATCAC 2081

RESULT 3  
V10266  
ID V10266 standard; cDNA to mRNA; 2837 BP.  
AC V10266;  
DT 03-JUN-1998 (first entry)  
DE Rat GABA-BR1b receptor cDNA.  
KW Gamma-aminobutyric acid; GABA-BR1b receptor; rat; brain; agonist;  
inhibitory neurotransmitter; peripheral nervous system; antagonist;  
treatment; dementia; depression; anxiety; bronchial inflammation; asthma;  
KW epilepsy; cognitive function; ds.  
OS Rattus norvegicus.  
FH Key Location/Qualifiers  
FT CDS 228..2762  
FT /tag=a  
FT /product= GABA-BR1b  
PN WO9746675-A1.  
PD 11-DEC-1997.  
PF 19-MAR-1997; E01370.  
PR 22-NOV-1996; US-756091.  
PR 30-MAY-1996; US-655716.  
PA (NOV) NOVARTIS AG.  
PI Bettler B, Bittiger H, Froestl W, Kaupmann K, Mickel SJ;  
DR WPI; 98-042183/04.  
DR P-PSB; W40118.  
PT Purified GABA-B receptor or receptor protein - and antagonists of  
PT these which may be useful in treating nervous system disorders  
PS Claim 3; Page 67-74; 108PP; English.  
CC This cDNA sequence encodes a novel rat GABA-B receptor protein.  
CC GABA-BR1b. GABA (gamma-aminobutyric acid) is the major inhibitory  
CC neurotransmitter found in the brain and peripheral nervous system  
CC and this receptor may be used for the identification of GABA-B  
CC receptor agonists and antagonists. Such proteins may be used in  
CC treatment of dementia, depression, anxiety, epilepsy, spasticity,  
CC bronchial inflammation or asthma or to improve cognitive function.  
CC GABA-B receptor ligands and probes derived from this sequence can be  
CC used to assay for GABA-B receptors or DNA encoding them  
SQ Sequence 2837 BP; 621 A; 842 C; 764 G; 610 T;

Query Match 12.1%; Score 342.4; DB 1; Length 2837;  
Best local similarity 49.7%; Pred. No. 4.5e-59;  
Matches 1128; Conservative 0; Mismatches 1091; Indels 51; Gaps 8;

QY 10 CCGCCGAGCTCCGCGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 69  
DB 207 CCG 266  
QY 70 CTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 129  
DB 267 CTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 326

QY 130 GCTC 189  
DB 327 CATCCCG 386  
QY 190 ACCAGAGGTGGCCAGAGGAGCATGGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 234  
DB 387 TACATCGGCG 446  
QY 235 GCGGTGAGCTAGCCATGAGCA---GATCCGCAAGAGTCACTCTGCGCCCTACTTC 291  
DB 447 GCGGTGAGATGGCGCTGAGAGAGCTTAACGCCGAGAGACATCTCTGCGGAGTACG 506  
QY 292 CTGAGCGTGGAGCTATGACACCGAGTGGACAAATGCAAGGAGGATGAAGACCTTCT 351  
DB 507 CTGAGCTTATTCACACGACGACGACGACGACGACGACGACGACGACGACGACG 566  
QY 352 GACGCAATTAAGTATGGCGCGGCAACATTTGATGCTGTTGGAGCGCTCTGCTGCTG 411  
DB 567 GAACTACTCTACAAATGACCCCATCAATCATCTCATGCTG---CTGATGTTCTGTC 623  
QY 412 ACATCTATTCAGGAGAGTCCCTCCAGGCTGGAATCTGTCAGCTTCCTGCGCGCG 471  
DB 624 TCCACACTTGTAGCTGAGGCTGCGCGGATGTGAACTTATGCTCTCATATGCTGCT 683  
QY 472 ACCAGCGCTGTTCTTGGCGATTAAGAAAGTACCCGATTTCTCCGAGCGGTGCGTCA 531  
DB 684 AGTTCAACAGCGCTTGTCAAAACCGACGCGTTTCCACGTTCTCCGAGCATCATC 743  
QY 533 GACAAAGCGGTGAAACCCCGCATCTGACCTCTGAGACATCTCCGCTGCGGCGT 591  
DB 744 GCAACACTCCAAATCCCAACCGCGGTGAACTTGTGAAAGGCGGCTGGAAGAGATC 803  
QY 593 GGCACACTCAGCGAGAGCTGACGCGCTTCCGAGGTGAGATGATGATGATGATGAT 651  
DB 804 GGTACATTCACAAACAGACACCGAGGCTTCCACCTCAACGCTGATGATGATGATG 863  
QY 653 CTGATGCGGAAATATTTAGATCTCAGACACAGAGATTTCTCCATATATCTCTGAC 711  
DB 864 GTGAAAGAGGCTGGATCGAGATCACTTCCGACAGAGTTCTTCCGATCAACGCTG 923  
QY 712 AGCGTCAAAAGCTCAAGGAGGATGACGTCGATCATCTTGGCAGTTTGACAGAT 771  
DB 924 CCTGTTAAACCTGGAAGGCTCAAGATGCTGATGATGATGATGATGATGATGATG 983  
QY 772 ATGCGACAAAGTCTTCTGTTGCTTGGCTTGAGAGAGCATGTTTGGCAGCAATGAC 831  
DB 984 GAAAGCCCGAAAGTCTTGTGAGCTTATAGAAAGGCTTCTTGGGAAAGTACGTC 1043  
QY 832 TCGATCATCCCGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 891  
DB 1044 TGGTCTCTCATCGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1103  
QY 892 TCGTACGCTGCTGCGAGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 951  
DB 1104 TGTAAAGT-----GGAAGAAATACCGAGCGGTGAGGCGGCACATCAACGAG 1154  
QY 952 TTTGAGCCCTGAGCTGCAAAATCAATCAAGACATGTCAGAGAGCTCAACGAGAT 1011  
DB 1155 ATGTGATGCTGAACCTGCGCAACACCGAAGATTTTCCAACTGACGTCACAGAA 1214  
QY 1012 GAAAGAGATCAACAGC-----AAAGTTCAAGCGGTGGGCGCCAGCAATTCATGG 1065  
DB 1215 GTGAGAAATCAACCAAGCGCTGAAAGACACCCGAGAGACTGAGAGCTTCCAGAG 1274  
QY 1066 TACGCTACATGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1125  
DB 1275 GCACCACTGGCTTATGATGCTATGATGCTTGGCTTGGCTTGAACAAGAGTGTGA 1334  
QY 1126 CATGCACTAGACAGCAACGAGATCCAGACTTCACTTCAACAGACCAACGCTGG 1185  
DB 1335 GAGGTGATGCTGCGGCTGCTGAGGAGCTTAACTTAACTTAACTTAACTTAACT 1394  
QY 1186 AAATATCTCTCAATGCTCAATGAGAGACCAACTTCTTGGGCTCAAGGCTCAAGT 1245

Db	1395	GACGAGATCTACGGGGCCATGAACTCCCTCTCTTGAGGGCGTTCTGGCCATGGTCT	1454
Qy	1246	TT---CCGGAACGGGGAGAAATGGGAACCATTTAAATTACTCAATTTCAAGCAGCA	1302
Db	1455	TTTGTATGCCACGGGCTCCGGATGGCATGACATTATTCAGACAGCTACAGGGCGGAGC	1514
Qy	1303	GAGGTGAAGTGGCGGAATCAACAGCGGGTGGTCAGACACTGGAGATATCATATGACAC	1362
Db	1515	TTCAGAAAGATCGGCTACTCGACACACACAAGATGATCTTCCTGGTCCAAAGCGAC	1574
Qy	1363	ATPAAGTTCCAGGGGTCGAGCCAGCCAGCAGCAAGCAACATCTCGGGAGCAGCTGG	1422
Db	1575	AAGTGAATGGAGGCT---TCCCCAGCTGACCAAGACTTGGTATCAGACATTCCT	1631
Qy	1423	AAGATCTCGCTTCCACTGTATAGCATCTGTCCGCTCAGCATCTCGGATGATATG	1482
Db	1632	TTCTGTCTCAGAAACTCTTATATCTCCGTCAATTCCTCCAGCCGTGGCATATGTCTT	1691
Qy	1483	GCGAGGGCTTCCTCTTCCATCTCAATCAAGAACCGGAACCAAAAGCTGATTAAGATGCA	1542
Db	1692	GCTGTGTCTGTCTGTCTTTAACTATCAACTCCACGCTGTTATATCCAGAACTCC	1751
Qy	1543	AGCCCCATATGAACAACCTCATCATCTGGGAGGAATGCTGTCTATGATCATCTTC	1602
Db	1752	CAGCCCCATCTGAACAATCTGACTGTGGGCTCTCTACAGCCAGCTGGTGTCTTC	1811
Qy	1603	CTCTTGGGCTCGATGGGTCCTTCTGTCTCAGAAAGACCTTGAACACTCTGACAGCTC	1652
Db	1812	CTCTTGGGCTGGATGGTATACACATAGGGAAGAACCGATTCCTCGTTGTCTGCCAGGCT	1871
Qy	1663	CGGACTGGATTTCTACCGTGGGCTACACAACTGCCCTTTGGGGCATATGTTGCAAGAC	1722
Db	1872	CGCTTTTGGCTCTTGGGCTTGGCTTTACTCTGGGCTATGGCTATATGTCACCAAGATC	1931
Qy	1723	TGAGAGTCTCATGCCATCTTCAAAAATGTGAAGATGAAGAA-----GAGATATATC	1773
Db	1932	TGTTGGTCTCACACAGTCTTCCAGAAAGAGGAGAAAGAGAGAGTGGAGGAAGACCTTA	1991
Qy	1774	AAGAGCCGAAGCTGCTTGTGATTTGGGGGGCATAGCTCATAGCACTGGTGGCATCTCG	1833
Db	1992	GACCCCTGGAAACTCTATGCCACTGTGGGCTGTGGTGGGATGGATGTCTGACTCTT	2051
Qy	1834	ATCTGTTTGGCAGGCTGTGGACCCCTGCGGAGAGACATAGAAGGTACACATGAGCCG	1893
Db	2052	GCCATGTGGCAGATGTGGACCCCTTGCACCAACCATTTGAGACTTTTGCAGAGGAGAA	2111
Qy	1894	GACCAGCAGCGCCGGGCAATCTCATCCGCCATTTGGTGGAACTGCGAAACACACCCAC	1953
Db	2112	CCAAAGGAAGATCATGATGTCTCATATTGCCCCACATTTGGAGCACTGCAACTCCAAAGAG	2171
Qy	1954	ATGACCATCTGGCTTGGCATTTGTCTACGGCTCTCAAGGGGCTCTCATATCTATTCGGTTGT	2013
Db	2172	ATGAAATACCTGGCTTGGCATTTTCTATATGTTTCAAGGGGCTGTGCTGTGGGATATC	2231
Qy	2014	TTCTTGGCATGTGGAAACCCGAAATGTAGATCCCGCCCTCAACGACACAGTATCATATC	2073
Db	2232	TTTCTTGTCTTAGGAACCAAGAGGTGTCTCACAGAAAAGATCATATGACACAGGCGGTG	2291
Qy	2074	GGCATAGTGTGTACATGTGGGATCATGTGCATCATCTGGGGCTGCTCTCTCTCTG	2133
Db	2292	GGCATAGCTATATCAAAATGTGCGGCTGTGTGTCTATCATCATCTGCTGTGACATATATC	2351
Qy	2134	ACCGTGCACACCCCAAGTGCATTTGTGATGTGGCCCTGGATCATCTTCTCAGC	2193
Db	2352	CTTTCAGTACAGAGAGAGCGCTTTGCTTTGCTCTGTGGCACTGTGTCTCTCTCC	2411
Qy	2194	ACCATCACTCTCGCTGTGTGTGTGTGTGCGCAAGCTATTAATCTGTAGAGAC	2243
Db	2412	TGATATCACTGTGTTGTCTTGTGTGTCACCAATATGCGCAGCTGATATAC	2461

ID V10264  
 ID V10264 standard: cDNA to mRNA; 4376 BP.  
 AC V10264:  
 DT 03-JUN-1998 (first entry)  
 DE Rat GABA-BR1A receptor cDNA.  
 KW Gamma-aminobutyric acid; GABA-BR1A receptor; rat; brain; agonist;  
 KW inhibitory neurotransmitter; peripheral nervous system; antagonist;  
 KW treatment; dementia; depression; anxiety; bronchial inflammation; asthma;  
 KW epilepsy; cognitive function; ds.  
 OS Rattus norvegicus.  
 FH Key Location/Qualifiers  
 FT CDS  
 FT 182..3064  
 FT /\*tag= a  
 FT /product= GABA-BR1A  
 FN W09746675-A1.  
 PD 11-DEC-1997.  
 PF 19-MAR-1997; E01370.  
 PR 22-NOV-1996; US-756091.  
 PR 30-MAY-1996; US-655716.  
 PA (NOVS ) NOVARTIS AG.  
 PI Bettler B, Bittliger H, Froestl W, Kaupmann K, Mickel SJ;  
 DR WPL: 98-042183/04.  
 DR P-PSDB: W40116.  
 PT Purified GABA-B receptor or receptor protein - and antagonists of  
 PT these which may be useful in treating nervous system disorders  
 PS Claim 3, Page 42-50; 108pp; English.  
 CC This cDNA sequence encodes a novel rat GABA-B receptor protein,  
 CC GABA-BR1A. GABA (gamma-aminobutyric acid) is the major inhibitory  
 CC neurotransmitter found in the brain and peripheral nervous system  
 CC and this receptor may be used for the identification of GABA-B  
 CC receptor agonists and antagonists. Such proteins may be used in  
 CC treatment of dementia, depression, anxiety, epilepsy, spasticity,  
 CC bronchial inflammation or asthma or to improve cognitive function.  
 CC GABA-B receptor ligands and probes derived from this sequence can be  
 CC used to assay for GABA-B receptors or DNA encoding them.  
 SO Sequence 4376 BP; 940 A; 1209 C; 1195 G; 1032 T;

## RESULT 4

Query Match	Similarity	Score	DB	Length
217	GGGCGCGCGCTGCTCCCGCCGCTGGAGCTAGCATCGAGCA--GATCGCCACGAGTCA	12.0%	339.6	4376
731	GGCCAGGCGCTCGACAGCCCGGCGTGAGATGGCGCTGGAGGAGCTTAAACAGCCACAGAC	50.4%	1.7e-58	
274	CTCTGTGGCCCTACTTCTTGAGCCCTGGAGCCCTATGTGACCGAGTGTGACAAATGCAAG	0	979	36
791	ATCTGCGCGGAGTACGAGTCAAGCTTATTCACCGACGACAAAGTGTGACCCAGGGCA	0	979	36
334	GGACTGAAGCCCTTCTATGACGCAATAAAGTATGGCGCCGAACCAATTTGATGTTTGA	0	910	36
851	GCCACCAAGTACTTGTACGAGTACTCTTCATATGACCCCATCAAGATCATCTTCATCTCT	0	910	36
394	GGCGTGTGCTCGCTGTGACATCTATATACGGGAGTCCCTCCAAAGCGTGAATCTGCTG	0	910	36
911	GG--CTGTAGTTCTGTCTCCACTTGTAGTGGTGGCTGCCCGAGTGTGAACCTTAT	0	910	36
454	CAGCTTCTCTTCCCGCGCACAGCCCTGTTTCTTGGGATGAAGAAGATACCGTATTTTC	0	910	36
968	GTGCTCTCATATGAGCTTCAGTTTACCAGGCTGTTCAAACGACAGCGGTTTCCACGCTTC	0	910	36
514	TTTCGGGAGGTGCGCTTCAGACAAAGCGGCTGAAACCCCGCATCTCGAAGCTTCGTAACAC	0	910	36
1028	TTTCGGGAGGATCCATCCGCGCACACTCCACATCCACCCCGGAGTAACTTTTGAAAAG	0	910	36
574	TTTCGGTGGGCGGTGTGGGACACTCAGACGAGAGCTGACGCGTCTCTCGAAGTGAAG	0	910	36
1088	TGGGCGTGAAGAAGATCGCTACCATTCGAACAGACACCGAGGCTTCCACTCAACGCTG	0	910	36
634	AATGACTGACTGGGGTCTCTGTATGGGGAAGATATTTGAGATCTCAGACACAGAGATTTTC	0	910	36
1148	GATGACTGGAAGGAGCGAGTGAAGAAGGCGCTGGAGATCGAGATCTTCTCGACAGATTTTC	0	910	36

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QY 694 TCCATATGTCCTGACACGCTCAAAAAGCTCAAGGGGATACGTGGGATCATCTT 753
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1208 TTCTCGATCCAGCTGTGCTCCGTTAAAACCTGAAGGCTCAAGATCTGAAATCTGG 1267
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 754 GGCAGCTTTGACCAAAATATGACAGCAAAAGCTCTGTTGTTGCTCTCCAGAGAGCATG 813
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1268 GGAATTTCTATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1327
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 814 TTGGCAGCAGTACAGTACGATCATCCGGGATGTTAGAGGCTGCTGGTGGGAGAGC 873
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Db 1328 TTGGGAGAGAGTACGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1387
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QY 874 GTGATGTGAGAGCCATTTCTCAGCTGCTGCGAGAGAGCCCTGCTGCTGCTGCTG 933
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Db 1388 TATGACCCGCTCAATCAATTTATGACAGTGA-----AATAATGACCGAGGGGGTGGAG 1438
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QY 934 GGTTCATTCGAGAGTGGATTTGAGCCCTGAGCTCCAAACAAATCAAGACATCTCAGGG 993
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Db 1439 GGCACATCCACGAGAGATTTGATGTCATGTAACCTGCAACACCGGAGGATTTTCAAC 1498
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 994 AAGATCCACAGCAGTATGAAGAAGATAGACA-----GCAAGCTTCAGGCTGAGG 1047
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1499 ATGACGTACAGGAATTTGTGAGAAACTAACAAGCGGCTGAAAAGACACCCGAGAGAG 1558
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QY 1048 CCCAGCAGTTCATGGGTACGCTCAGATGAGATCTGGGTCTATGGCCAGAGACCTCAG 1107
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Db 1559 ACTGAGGCTTCTCAGAGAGGACCACTGCGCTATGATGATCTTATGAGGCTTGGCTTGGCC 1618
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1108 AGGCCATGAGAGACACTGATGAGCAGTACAGGACGAGGAGTACAGGACTTCATCTAC 1167
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Db 1619 TTGAACAAGAGCTGTGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1678
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1168 AAGAGCAGCAGCTGGGCAAAATCATCTCTCATGCTGTAACAGAGACCAACTCTTCGGG 1227
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Db 1679 AACAGCCAGACCTTACAGACCAAGTCTACCGGCGCATGAACTCTCTCTTGAAGGCG 1738
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QY 1228 GTACAGGGTCAAGTGTGTCGG---AACGGGAGAGAAATGGGAAACATTAATTTACT 1284
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Db 1739 GTTCTGCGCATGTGCTTGTATGACAGCGGCTCCGAGTGGACATGACATTAATCAGAG 1798
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1285 CAATTTCAAGCAGCAGAGAGAGTGAAGTGGGAGTGAACAGCGGAGTGGTGCATACAG 1344
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1799 CAGCTACAGGCGGAGCTACAGAAAGTGGCTACTACAGCAGCAGCAGCAGCAGCAGCAG 1858
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1345 GAGATCATCATGACACCATTAAGTTCAGAGGCTCGAGGCCACCCAGACAGCAAGACCATC 1404
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Db 1859 TCTGTGCTCAAAAGCAGCAAGTGTGAGAGGCTCTCCAGC---TGACACGAGACTTG 1915
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1405 ATTCTGAGAGCACTTGGAGAAATCTCGCTTCCATGTATGATCCGTGCTGCTGCTGCTG 1464
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1916 GTATCAAGACATTCCTGTTCTGTCTAGAAACTCTTATCTTCCTGCTGCTGCTGCTGCTG 1975
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1465 ATCTCGGAGTATCATGAGCGGCTTCTCTCTTCTTCAACATCAAGACCGGAAACCA 1524
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Db 1976 AGCTGTGGAGTGTCTGCTGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTG 2035
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QY 1525 AAGCTGATAGATGTCAAGCCCTACATGAAACCACTCATCTCCAGGAGGATGCTG 1584
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Db 2036 CCTTATTCAGAACTCCAGGCGCAACTGAACTGACTGTGTGTGTGTGTGTGTGTGTGTG 2095
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QY 1585 TCTATGATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1644
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QY 1645 GAAACACCTGTGAGGTCGGGACCTGATCTTCAACCGTGGGCTTCAACACTGCTTGGG 1704
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Db 2156 CCGTTGTGTGCGCAGGCGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2215
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Db 2216 TCTATGTTCCACCAAGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2275
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QY 1764 -----GAATCATCAAGACCAAGAGAGCTGCTGTGATGTGGGGGAGCATGCTGCTC 1815
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2276 GAGTGGAGGAGAGACCTTAGAGAGCTGGAAACTTATGCACTGTGTGGCTGTGTGGCC 2335
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1816 ATGACCTGTGATCTGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 1875
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2336 ATGATGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 2395
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1876 AGGTACAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1935
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2396 ACTTTTGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2455
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1936 CACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1995
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2456 CACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2515
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1996 CTGATGCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2055
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2516 CTGCTGCTGCTGAGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2575
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2056 AAGCAGCAGAGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2115
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2576 AATGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2635
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2116 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2175
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2636 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2695
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2176 GTGATCATCTTCTGAGAGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2235
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2696 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2755
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2236 CTGAGGAC 2243
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2756 CTGATCAC 2763
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 5

V88919

ID V88919 standard; cDNA; 314 BP.

AC V88919;

DE 12-FEB-1999 (first entry)

DE EST clone HM456

KW Expressed sequence tag; secreted protein; haematopoiesis regulator;

KW tissue growth; activin; inhibin; tumour invasion suppressor; EST; human;

KW chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;

KW receptor; ligand; anti-inflammatory; tumour inhibitor; ds.

OS Homo sapiens.

PN M09845437-A2.

PD 15-OCT-1998.

PE 10-APR-1998: U06956.

PR 10-APR-1997: US-837312.

PA (GENE ) GENENTICS INST INC.

PI Agostino WJ, Jacobs K, Lavalie ER, McCoy JM, Merberg D,

PI Racine LA, Spaulding V, Treacy M;

DR WPI; 99-070078/06.

PT New polynucleotides encoding human secreted proteins - derived from

PT e.g. human blood, kidney, foetal lung, placenta, testes, brain,

PT ovary, pituitary, retina and colon cDNA libraries

PS Claim 1: Page 556-557; 64pp; English.

CC The present sequence represents an expressed sequence tag (EST), and is

CC a polynucleotide of the invention. The polynucleotides of the invention

CC are all secreted EST sequences isolated from a variety of human tissue

CC sources. The EST sequences and proteins encoded by them are predicted to

CC have useful biological activities which would make them suitable for

CC treating, preventing or ameliorating medical conditions in humans and

CC animals, although no supporting data is given. Suggested activities

CC include nutritional activity, immune stimulating or suppressing activity,

CC haematopoiesis regulating activity, tissue growth activity,

CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic

CC and thrombolytic activity, chemotactic/chemokinetic activity, anti-inflammatory

CC activity, cadherin/tumour invasion suppressor activity, tumour inhibition

CC activity. The EST sequences are also stated to be useful for gene

CC therapy. 314 BP; 72 A; 81 C; 89 G; 72 T;  
SQ Sequence

Query Match 8.6%; Score 241.6; DB 1; Length 314;  
Best Local Similarity 87.2%; Pred. No. 2.3e-39;  
Matches 265; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 1733 ATGCCATCTTCAAAATGTAGATGAGAGAAAGATCATCAAGACAGACAGCTGCTG 1792  
DB 3 ATTCGGCCCTTACATGCGCTAGAAAATGAAAGAAAGATCATCAAGGACCAAACTCTTG 62  
QY 1793 TGATGTGGGGGGGATGCTGCTCATGACCTGTGCATCTGATCTGTGTGGAGCTGTG 1852  
DB 63 TGATGTGGGGGGGATGCTGCTCATGACCTGTGTATCTGATCTGTGACAGCTGTG 122  
QY 1853 ACCCCCTCGGAGAGAGTAGAGAGTACATGAGACCGGACCCAGCAGCGCGGACA 1912  
DB 123 ACCCCCTCGGAGAGAGTAGAGAGTACATGAGACCGGACCCAGCAGCGGATA 182  
QY 1913 TCTTCATCCGCCCATTTGCTGGAAGACTGCGAAAACACCCACATGACATCTGGCTTGCA 1972  
DB 183 TCTTCATCCGCCCATTTGCTGGAAGACTGCGAAAACACCCACATGACATCTGGCTTGCA 242  
QY 1973 TTGCTACGCGCTACAGGGGGCTCCTCATGCTATCGGTTGTTCTTGATGGAGAACCC 2032  
DB 243 TCGTCTATGCTTACAGAGGACTTCTCATGTTGTTGTTGTTTCTTAGCTTGGAGAACCC 302  
QY 2033 GCAA 2036  
DB 303 GCAA 306

RESULT 6  
X51891  
ID X51891 standard; DNA: 361 BP.  
AC X51891:  
DE 22-JUN-1999 (first entry)  
DE Human secreted protein 5; EST SEQ ID NO: 105.  
DE Human; secreted protein; EST; expressed sequence tag; diagnosis;  
KW forensic; gene therapy; chromosome mapping; signal peptide;  
KW upstream regulatory sequence; cytokine activity; cell proliferation;  
KW differentiation; haematopoiesis regulation; tissue growth regulation;  
KW reproductive hormone regulation; chemotactic; chemokine; haemostatic;  
KW thrombolytic; anti-inflammatory; tumour inhibition; ds.  
OS Homo sapiens.  
PN WO9906552-A2.  
PD 11-FEB-1999.  
PE 31-JUL-1998; IB1236.  
PR 01-AUG-1997; US-905223.  
PA (GDSR) GENSET.  
PI Duclert A, Dumas M,line Edwards J, Lacroix B;  
DR P-PDB; Y13091.  
PT New isolated brain-derived nucleic acids - used to develop products  
PT which may have cytokine, immune, regulatory, haematopoiesis  
PT regulating, anti-inflammatory or tumour inhibition activity  
PS Claim 1; Page 253; 577pp; English.  
CC X51891 to X52019 represent 5' expressed sequence tags (ESTs) for human  
CC secreted proteins, and encode the proteins given in Y1297 to Y13219,  
CC respectively. The proteins given represent the signal peptide and an  
CC N-terminal fragment of a secreted protein. The nucleic acid sequences  
CC can be used for producing secreted human gene products. They can also  
CC be used to develop products for diagnosis and therapy. The proteins  
CC obtained may have cytokine activity, cell proliferation/differentiation  
CC activity, haematopoiesis regulating activity, tissue growth regulating  
CC activity, reproductive hormone regulating activity, chemotactic/  
CC chemokinetic activity, haemostatic and thrombolytic activity, receptor/  
CC ligand activity, anti-inflammatory activity, tumour inhibition activity  
CC or other activities. The products can be used in forensic, gene therapy  
CC and chromosome mapping procedures. The sequences can also be used for  
CC obtaining corresponding promoter sequences. The nucleic acids encoding  
CC the signal peptide can be used for directing extracellular secretion of

CC a polypeptide or the insertion of a polypeptide into a membrane, or  
CC importing a polypeptide into a cell.  
CC Sequence 361 BP; 86 A; 89 C; 94 G; 92 T;  
SQ Sequence

Query Match 5.1%; Score 143.4; DB 1; Length 361;  
Best Local Similarity 80.4%; Pred. No. 5.4e-20;  
Matches 168; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 287 ACTTCTGGAGCTGGAGCTCATGACACCGAGTGTGACATGCAAGGAGTGAAGCCT 346  
DB 153 AGTCATCTATTGTTGGAGCGCATATCATGTAGTGACACGCAAAAGGTTGAAGCCT 212  
QY 347 TCTATGACCAATAAGATGATGGCCGAACCATTTGATGTTGAGGCGCTGTGCGT 406  
DB 213 TCTATGATGATATAAATAAGCGGCTTACCACTGATGTTGAGAGCGCTGTGCAAT 272  
QY 407 CTTGACATCTATTATCGGAGATCCTTCGAAGCTGGAATCTGTGACGTTTCTTCG 466  
DB 273 CCGTACATCTCATATTCAGAGTCCCTCCAAAGGCTGGAATCTGTGACGTTTCTTCG 332  
QY 467 CCGCAACACGCGCTGTCTTGGGATAG 495  
DB 333 CTGCAACACGCGCTGTCTTAGCCGATAG 361

RESULT 7  
027091/C  
ID 027091 standard; DNA: 1028 BP.  
AC 027091:  
DE 25-JAN-1993 (first entry)  
DE XTY26 probe.  
KW Fragile X locus; replacement therapy; (CCG)n repeat; Xq27.3;  
KW Cpg island; ss.  
OS Homo sapiens.  
PN WO9212262-A.  
PD 23-JUL-1992.  
PE 03-JAN-1992; U00020.  
PR 04-JAN-1991; US-638518.  
PR 20-MAR-1991; US-672232.  
PR 06-DEC-1991; US-802650.  
PA (ADEL-) ADELAIDE MEDICAL CENT WOMEN & CHILDREN.  
PI (UNIW) UNIV WASHINGTON.  
PI NagaraJa R, Richards R, Schlessinger D, Sutherland GR;  
DR MPI: 92-268680/32.  
PT DNA spanning the Fragile X site on the human X chromosome - for  
PT diagnosis and treatment of associated mental retardation  
PS Claim 8; Page 23; 47pp; English.  
CC This sequence or an effective fragment of it, may be used as a probe  
CC for the human Fragile X locus. This probe crosses the fragile site  
CC and can be seen to be useful in replacement therapy. Affected  
CC individuals appear to have an amplification of a (CCG)n repeat  
CC sequence at the fragile site which gives a band of a different size  
CC than a normal individual when Southern blots are probed with this  
CC probe. The fragile site occurs at the Xq27.3 locus on the X-  
CC chromosome. It is in the immediate proximity of a Cpg island and is  
CC therefore thought to interfere with the expression of a gene or the  
CC function of its' product, this is thought to be the molecular  
CC basis of the disease.  
SQ Sequence 1028 BP; 128 A; 327 C; 412 G; 161 T;

Query Match 2.2%; Score 63.4; DB 1; Length 1028;  
Best Local Similarity 63.4%; Pred. No. 0.00039;  
Matches 97; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 3 GCGTTCCTCCGCGGAGCTCGGGGAGCCCGCGCGCGCGCGCGCGCGCGCGCGCG 62  
DB 463 GCG 404  
QY 63 CTTCTGCTGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 122  
DB 403 GCG 344



Oy	123	GACCGGAGGGCCCCCCCCCCCCCAGAG	155
Dd	343	CCCGCCCCCGCTCACAGAGCGGCCCTCCACCGG	311
RESULT	8		
ID	051731/c		
AC	051731;		
DE	31-MAY-1994 (first entry)		
DR	Plasmid pCiSEBON for subcloning hNHGF variants.		
KM	Hepatocyte Growth Factor; HGF; variant; muteth; in vitro mutagenesis		
KW	proteolysis resistant; liver; malignancy; CMV-driven;		
KW	Cytomegalovirus; episomal expression plasmid; ss.		
OS	Synthetic.		
FH	Key	Location/Qualifiers	
FT	enhancer	1..611	
FT		/tag= a	
FT		/note= "CMV enhancer/promoter"	
FT	promoter	758..775	
FT		/tag= b	
FT		/label= Sp6_promoter	
FT	misc_feature	845..849	
FT		/tag= c	
FT		/note= "Sp6 RNA start"	
FT	misc_feature	902..966	
FT		/tag= d	
FT		/function= cloning_linker	
FT	polya_signal	967..1107	
FT		/tag= e	
FT		/note= "SV40 poly A"	
FT	misc_feature	1108..1531	
FT		/tag= f	
FT		/function= SV40_Origin	
FT	misc_feature	1580..4189	
FT		/tag= g	
FT		/label= EBNA-1	
FT	misc_feature	4190..6374	
FT		/tag= h	
FT		/function= orip	
FT	repeat_region	4295..4887	
FT		/tag= i	
FT		/note= "family of repeats"	
FT	misc_structure	5866..5978	
FT		/tag= j	
FT		/note= "dyad region"	
FT	terminator	6375..6457	
FT		/tag= k	
FT		/label= HSV_TK_terminator_3'-end	
FT	cds	6975..7975	
FT		/tag= l	
FT		/phenotype= neomycin_resistance	
FT		/note= "fus neomycin phosphotransferase gene"	
FT	promoter	7975..8112	
FT		/tag= m	
FT		/label= TK_Promoter	
FT	misc_feature	8114..8594	
FT		/tag= n	
FT		/function= M13_ori	
FT	misc_rna	8595..10414	
FT		/tag= o	
FT		/label= delta_2a	
PT	WO9323541-A.		
PD	25-NOV-1993.		
PF	17-MAY-1993.	U04648.	
PR	18-MAY-1992; US-884811.		
PR	18-MAY-1992; US-885971.		
PA	(GETH ) GENENTECH INC.		
PI	Godowski PJ, Lokker NA, Mark MR:		
DR	WPI: 93-386573/48		
PT	Hepatoocyte growth factor variants - are resistant to proteolytic cleavage into its two-chain form, used to treat malignancies		

	Pt	associated with HGF receptor
	PS	Example 1; Fig 6; 87bp; English.
	CC	Plasmid pcISEBON (a pRK5 derivative) is an episomal CMV driven
	CC	expression plasmid. hnhGF variants with enhanced receptor binding
	CC	activity were produced by site-directed mutagenesis. Stable
	CC	populations of preferred HGF variants were obtained by transfecting
	CC	human embryonic kidney 293 cells and then these were subcloned in
	CC	pcISEBON. See R32940-R52949 for examples of pref. HGF variants.
	SC	Sequence 10596 BP; 2625 A; 2571 C; 3024 G; 2376 T;
	Query Match	2.1%; Score 59.8; DB 1; Length 10596;
	Best Local Similarity	50.5%; Pred No. 0.003;
	Matches 145;	Conservative 0; Mismatches 142; Indels 0; Gaps 0
Oy	20	CGGAGCAGCCCCGGCGCGCGCGCGCGCGCGCGCGCGCGCTGTGCCTGC 79
Db	2614	CCCTTCGCTCTCTGCGCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2555
Oy	80	TGCTGTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 139
Db	2554	TCTGTGCCCT 2495
Oy	140	GACGCGCGCCAGCAGCGCCGCGCTCTCATATGAGGCGCTATGCGGCTCAACAAGAGG 199
Db	2494	TGCTCTGCGCCCT 2435
Oy	200	TGGGCAAGGGAGCATGTGGGCGGGGCTCTCCCGCGGTGGAGTAGCAATGACAGA 259
Db	2434	TGCCCCCT 2375
Oy	260	TCCGCAAGCATCT 306
Db	2374	TCTGCGCCCT 2328
	RESULT 9	
ID	T40348 standard; DNA; 10596 BP.	
ID	T40348/C	
AC	09-DEC-1996 (first entry)	
DE	Human; pcISEBON for expression of hepatocyte growth factor.	
KW	plasmaid; hepatocyte growth factor; HGF; hnhGF; serum; proteolytic cleavage;	
KM	pro-hormone; beta subunit; alpha subunit; kringle domain; prothrombin;	
KW	plasmonogen; catalytic domain; serine protease; HGF variant;	
KX	HGF receptor; malignancy; chronic HGF receptor activation; ss.	
OS	Synthetic.	
PN	US5547856-A.	
PD	20-AUG-1992.	
PF	18-MAY-1992; 884811.	
PR	18-MAY-1992; US-885971.	
PR	18-MAY-1992; US-884811.	
PR	13-JUL-1993; US-087783.	
PPA	(GETH.) GENENTECH INC.	
PI	Godowski PJ, Lokker NA, Mark MR;	
WPt	96-392634/39.	
DR	New hepatocyte growth factor variants - are resistant to in vivo	
PT	proteolytic cleavage into a 2-chain form, useful as HGF antagonists	
PS	Example 1; fig 6; 39pp; English.	
CC	This sequence represents the episomal CMV driven expression plasmid	
CC	pcISEBON which was used in the expression of variant human hepatocyte	
CC	growth factor (HGF). HGF is isolated from human serum and is a	
CC	disulphide linked heterodimer derived by proteolytic cleavage of the	
CC	pro-hormone between residues 494 and 495. This generates a molecule	
CC	composed of an alpha subunit of 440 amino acids (mol. wt. 69 kD) and	
CC	a beta subunit of 234 amino acids (mol. wt. 34 kD). The alpha and beta	
CC	contants are encoded by a single open reading frame. The alpha subunit	
CC	contains four kringle domains based on their homology to kringle-like	
CC	domains in other proteins, e.g. prothombin, plasminogen. The beta	
CC	subunit shows high homology to the catalytic domain of serine proteases.	
CC	However two of the three residues which form the catalytic triad of	
CC	serine proteases are not conserved in HGF. Therefore, the precise	
CC	function of the beta chain remains unknown. The invention includes HGF	









Tue Mar 21 10:26:23 2000

Db 81 GCTGCTGCCCCGCGGCCCCCGGAGCGGGAGCCGCCCTTCCCCGGCTCGCCGCGC 140  
QY 147 GCCCAGCAGCCCCGCGCTCTCCATCATGGCCCTCATGCCGC 187  
Db 141 GCTGAGCCTGCGCCCCCTCGCGGAGCGGGGCTGGAGCTGC 181

Search completed: March 16, 2000, 17:43:01  
Job time: 3925 sec











RESULT 9  
 US-08-599-654-7  
 Sequence 7, Application US/08599654  
 Patent No. 5882925  
 GENERAL INFORMATION:  
 APPLICANT: FALB, DEAN A  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
 TITILE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
 NUMBER OF SEQUENCES: 54  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: PENNIE & EDMONDS  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10036-2711  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/599,654  
 FILING DATE: 09-FEB-1996  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/485,573  
 FILING DATE: 07-JUN-1995  
 PRIOR APPLICATION DATA: US 08/386,844  
 APPLICATION NUMBER: US 08/386,844  
 FILING DATE: 10-FEB-1995

```

1  TITLE OF INVENTION:  Inhibition of the Mitogenic Activity o
2  TITLE OF INVENTION:  pgcf by Mammalian EGR
3  NUMBER OF SEQUENCES:  12
4  CORRESPONDENCE ADDRESS:
5  ADDRESSEE:  Campbell and Flores
6  STREET:  4370 La Jolla Village Drive, Suite 700
7  CITY:  San Diego
8  STATE:  California
9  COUNTRY:  USA
10 ZIP:  92122
11
12  COMPUTER READABLE FORM:
13  MEDIUM TYPE:  Floppy disk
14  COMPUTER:  IBM PC compatible
15  OPERATING SYSTEM:  PC-DOS/MS-DOS
16  SOFTWARE:  Patentn Release #1.0 , Version #1.25
17
18  CURRENT APPLICATION DATA:
19  APPLICATION NUMBER:  US/08/224,482
20  FILING DATE:  07-APR-1994
21  CLASSIFICATION:  435
22
23  ATTORNEY/AGENT INFORMATION:
24  NAME:  Campbell, Cathryn A.
25  REGISTRATION NUMBER:  31,815
26  REFERENCE NUMBER:  P-ME 9913
27  TELECOMMUNICATION INFORMATION:
28  TELEPHONE:  (619) 535-9001
29  TELEFAX:  (619) 535-8949
30  INFORMATION FOR SEQ ID NO:  3 :
31  SEQUENCE CHARACTERISTICS:
32  LENGTH:  3132 base pairs
33  TYPE:  nucleic acid
34  STRANDEDNESS:  double
35

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: March 19, 2000, 16:24:44 ; Search time 2783.46 Seconds  
(without alignments)  
-3538.772 Million cell updates/sec

Title: US-09-211-755-1  
Perfect score: 3244  
Sequence: 1 TGACCTCGGGCAGGTCCTG.....CTTGCAAAAAAAAAAAAAA 3244

Scoring table: IDENTITY\_NUC

Searched: 821193 seqs, -1518192014 residues

Database : GenEmbl.\*

Word size : 0

Number of hits that pass the threshold : 1642386

- 1: gb\_ba1.\*
- 2: gb\_ba2.\*
- 3: gb\_om.\*
- 4: gb\_ov.\*
- 5: gb\_pat.\*
- 6: gb\_ph.\*
- 7: gb\_pl1.\*
- 8: gb\_pl2.\*
- 9: gb\_pr1.\*
- 10: gb\_pr2.\*
- 11: gb\_pr3.\*
- 12: gb\_ro.\*
- 13: gb\_sts.\*
- 14: gb\_sy.\*
- 15: gb\_un.\*
- 16: gb\_vl.\*
- 17: em\_fun.\*
- 18: em\_hum1.\*
- 19: em\_hum2.\*
- 20: em\_in.\*
- 21: em\_om.\*
- 22: em\_or.\*
- 23: em\_ov.\*
- 24: em\_pat.\*
- 25: em\_ph.\*
- 26: em\_pl.\*
- 27: em\_ro.\*
- 28: em\_sts.\*
- 29: em\_sy.\*
- 30: em\_un.\*
- 31: em\_vl.\*
- 32: gb\_htg1.\*
- 33: gb\_htg2.\*
- 34: gb\_in1.\*
- 35: gb\_in2.\*
- 36: em\_ba1.\*
- 37: em\_ba2.\*
- 38: em\_hum3.\*
- 39: em\_hum4.\*
- 40: gb\_pr4.\*
- 41: gb\_htg3.\*
- 42: gb\_htg4.\*
- 43: gb\_htg5.\*
- 44: gb\_htg6.\*
- 45: gb\_htg7.\*
- 46: em\_htg1.\*
- 47: em\_htg2.\*
- 48: em\_htg3.\*
- 49: em\_hum5.\*

50: gb\_pl3.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2964.8	91.4	5786	11	AF056085	Homo sapi
2	2961.6	91.3	3155	40	AF099033	AF099033 Homo sapi
3	2928.6	90.3	3240	40	AF095784	AF095784 Homo sapi
4	2752.2	84.8	3075	40	AF069755	AF069755 Homo sapi
5	2664	82.1	2826	40	AF074483	AF074483 Homo sapi
6	2659.2	82.0	2826	10	HS012188	AF012188 Homo sapi
7	2308.2	71.2	3288	12	AFI09405	AFI09405 Rattus no
8	2308.2	71.2	5614	12	RN0011318	AF011318 Rattus no
9	2304.2	71.0	5459	12	AF058795	AF058795 Rattus no
10	2218.2	68.4	2823	12	AF074482	AF074482 Rattus no
11	655	20.2	743	11	AF095723	AF095723 Homo sapi
12	649	20.0	740	11	AF095724	AF095724 Homo sapi
13	454	14.0	465	9	AB015334	AB015334 Homo sapi
14	448	13.8	153790	42	AC011957	AC011957 Homo sapi
15	400.8	12.4	3989	35	AF145639	AF145639 Drosophill
16	317.2	9.8	2928	9	HS0225029	AJ225029 Homo sapi
17	317.2	9.8	2535	10	HS012186	AJ012186 Homo sapi
18	315.2	9.7	4481	9	HS012288	AJ012288 Homo sapi
19	315.2	9.7	4445	9	HS0225028	AJ225028 Homo sapi
20	315.2	9.7	2886	10	HS012185	AJ012185 Homo sapi
21	315.2	9.7	2700	10	HS012187	AJ012187 Homo sapi
22	313.6	9.7	3192	40	AF099148	AF099148 Homo sapi
23	312.8	9.6	3202	12	AB016161	AB016161 Rattus no
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27	296.4	9.1	4365	12	AF114168	AF114168 Mus muscu
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ACCESSION AF056085  
VERSION AF056085.1 GI:3719225  
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SOURCE human.  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 5786)

## AUTHORS

Clark, J.C., Lam, A. and Bonner, T.I.

## TITLE

gb2, a second GABA-B receptor

## JOURNAL

Unpublished

## REFERENCE

2 (bases 1 to 5786)

## AUTHORS

Clark, J.C., Lam, A. and Bonner, T.I.

## TITLE

Direct Submission

## JOURNAL

(27-MAR-1998) Section on Genetics, NIMH, Bldg 36, Rm

## FEATURES

3D06, MSC 4094, Bethesda, MD 20892-4094, USA

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REFERENCE 1 (bases 1 to 3155)
AUTHORS Martin,S.C., Russek,S.J. and Farb,D.H.
TITLE Molecular identification of the human GABABR2: cell surface
expression and coupling to adenylyl cyclase in the absence of
GABABR1
JOURNAL Mol. Cell. Neurosci. 13 (3), 180-191 (1999)
MEDLINE 99263199
REFERENCE 2 (bases 1 to 3155)
AUTHORS Martin,S.C., Russek,S.J. and Farb,D.H.
TITLE Direct Submission
JOURNAL Submitted (15-OCT-1998) Laboratory of Molecular Neurobiology,
Department of Pharmacology, Boston University School of Medicine,
715 Albany Street, L606, Boston, MA 02118-2394, USA

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ACCESSION AF095784  
VERSION AF095784.1 GI:4836217  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 3240)  
AUTHORS Liu, M., Parker, R., McCrea, K., Watson, J., Baker, E., Sutherland, G.  
and Herzog, H.  
TITLE Cloning and characterization of a novel human GABA-B receptor  
subtype with high affinity for GABA and low affinity for baclofen  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 3240)  
AUTHORS Liu, M., Parker, R., McCrea, K., Watson, J., Baker, E., Sutherland, G.  
and Herzog, H.  
TITLE Direct Submission  
JOURNAL Submitted (15-NOV-1998) Neurobiology Program, Garvan Institute of  
Medical Research, 384 Victoria St, Sydney, NSW 2010, Australia  
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BASE COUNT 782 a 958 c 867 g 633 t

Query Match 90.3%; Score 2928.6; DB 40; Length 3240;  
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DB	1134	CCACACGATATGAGAGAGTACAACAAGCGGTGAGCGGTGGGGCCCGCCAGCAAGTTC	1193
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DB	1254	ACATGTCATCCAGCAGCCGCCACCGAGCGATCCAGGACTTCAACTACAGGACACACG	1313
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VERSION	AF069755.1	GI:4091932		
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Eutheria; Primates; Catarrhini; Homidae; Homo.				
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Ng,G.T.K., McDonald,T., Bonner,T., Rigby,M., Heavens,R.,				
Whiting,P., O'Neill,G.P. and Liu,Q.				
Evans,J., O'Neill,G.P. and Liu,Q.				
Cloning of a novel G-protein-coupled receptor GPR 51 resembling				
GABAB receptors expressed predominantly in nervous tissues and				
mapped proximal to the hereditary sensory neuropathy type 1 locus				
on chromosome 9				
Genomics 56 (3), 288-295 (1999)				
2 (bases 1 to 3075)				
McDonald,T. and Liu,Q.				
Direct Submission				
Submitted (03-JUN-1998) Human Genetics, Merck Research Labs, West				
Point, PA 19486, USA				
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REFERENCE 1 (bases 1 to 2826)  
AUTHORS Borowsky,B., Laz,T. and Gerald,C.  
TITLE Direct Submission  
JOURNAL Submitted (25-JUN-1998) Department of Molecular Biology, Synaptic  
Pharmaceutical Corporation, 215 College Road, Paramus, NJ 07652,  
USA  
2 (bases 1 to 2826)  
AUTHORS Borowsky,B., Laz,T. and Gerald,C.  
TITLE Direct Submission  
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1 (bases 1 to 2826)  
White, J.H., Wise, A., Main, M.J., Green, A., Fraser, N.J., Disney, G.H.,  
Barnes, A.A., Emsom, P., Foord, S.M. and Marshall, F.H.  
Heterodimerization is required for the formation of a functional  
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Nature 396 (6712), 679-682 (1998)  
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Fraser, N.J.  
Direct Submission  
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DEFINITION AF109405
VERSION AF109405.1 GI:4107514
KEYWORDS
SOURCE
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE
1 (bases 1 to 3288)
Kuner, R., Kohr, G., Grunewald, S., Eisenhardt, G., Bach, A. and
Kornau, H.-C.
Role of heteromer formation in GABAB receptor function
JOURNAL
MEDLINE
99102694
REFERENCE
2 (bases 1 to 3288)
Kuner, R., Kohr, G., Grunewald, S., Eisenhardt, G., Bach, A. and
Kornau, H.-C.
Direct Submision
Submitted (25-NOV-1998) Department of Neuroscience, BASF-LYNX
Bioscience AG, Im Neuenheimer Feld 515, Heidelberg D-69120, Germany
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Pharma AG, CH-125 6-20, CH-4002 Basel, SWITZERLAND  
REFERENCE 2 (bases 1 to 5614)

AUTHORS Kaupmann,K., Malitschek,B., Schuler,V., Heid,J., Froestl,W.,  
Beck,P., Mosbacher,J., Bischoff,S., Kulik,A., Shigemoto,R.,  
Karschin,A. and Bettler,B.  
TITLE GABA(B)-receptor subtypes assemble into functional heteromeric  
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JOURNAL Nature 396 (6712), 683-687 (1998)  
MEDLINE 99087322  
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Q	937	AGTAAATATAGTGGATCATTCGGGCTGTGACGAGCCTTCTTGGTGGGACAGTCCAC	996
D	1103	AGCAAGTACCAAGTGGATCATCCCGGGATGTACGAGCCGCTGTGTGGGACAGTGCAT	1162
Q	997	ACGGAACCAACATCAACCCGCTCCCTCCGGGAAGATCTGCTGCTGCCATAGAGGCTAC	1056
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D	1223	ATGGAGTGGACTTTGAGCCCTGAGCTCTCCAAACAAATTAACCATCTCAGGAAAGCT	1282
Q	1117	CCACAGCAGTATGAGAGAGATGACAAACAAACAGCGTCAAGCGTGGGCCCCAGCAAGTTC	1176
D	1283	CCACAGCAGTATGAAAGAGATGACAAACAAACGTTCAAGCGTGGGCCCCAGCAAGTTC	1342
Q	1177	CAGCGGTACGCTTACGATGGCATCTGGGTATCTGCCAANACACTGCAGAGGGCCATGGAG	1236
D	1343	CATGGGTACGCTTACGATGGGATCTGGGTATCTGCCAANACACTGCAGAGGGCCATGGAG	1402
Q	1237	ACACTGCATGCCAGACACCGGACACAGCGGATCCAGAGATTCAATACGAGCACACAG	1296
D	1403	ACACTGCATGCCAGTACGAGGACACAGCGGATCCAGAGATTCAATACGAGCACACAG	1462
Q	1297	CTGGGACGAGTCACTCTCAATGGCATGAACGAGACCACTTTCGGGGGTCAAGGGTCAA	1356
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Q	1357	GTTGTATTCCGGGAATGGGGAGAAATGGGGACATTAAATTACTCATTTCAAGACACG	1416
D	1523	GTTGTATTCCGGGAACGGGGAGAAATGGGAACCTTAAATTACTCAATTTCAAGACACG	1582
Q	1417	AGGAGGTGAAGGTGGGAGATCAACAGCGTGTGGCCGACACACTGAGATCATCAATGAC	1476
D	1583	AGAGAGGTGAAGGTGGCGGAAATCAACAGCGGTGTGACACACTGAGATCATCAATGAC	1642
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D	1883	TTTCTCTTTGGCTCTGATGGGTCTTCTGCTCGAAAAGACCTTTGAAAACACTCTGCAC	1942

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OY	1837	ACCTGAGACGTCCAGGCCATCTTCAAAAATGTGAAATGAAGAAGATCATCAAGAC	1896
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Db	2243	ATCTGGCTTGGCATCTGTATAGCCCTACAAAGGGGCTCCCTCATGCTATTCGGTTGTTCTTG	2302
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Db	2423	GACGAGGCCAAGTGCATGTGCAATGCTGGGCTGTGGTCACTCTTGTGAGCAACATC	2482
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Db	2483	ACTCTGTGCTGTGTTTGTGGCAAAAGCTCATCACTGTGAGAGCAAAACCTGAGCAAGC	2542
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RESULT	9			
LOCUS	AF058795	5459 bp	mRNA	ROD
DEFINITION	Rattus norvegicus GABA-B receptor gb2 mRNA,			15-OCT-1998
ACCESSION	AF058795			complete cds.
VERSION	AF058795.1	GI:3746525		
KEYWORDS	.			
SOURCE	Norway rat.			
ORGANISM	Rattus norvegicus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
AUTHORS	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
TITLE	1 (Bases 1 to 5459)			
JOURNAL	Clark,J.C., Lam,A. and Bonner,T.I.			
REFERENCE	gb2, A second GABA-B receptor			
AUTHORS	Unpublished			
TITLE	2 (Bases 1 to 5459)			
JOURNAL	Clark,J.C., Lam,A. and Bonner,T.I.			
FEATURES	Direct Submission			
	Submitted (09-APR-1998) Section on Genetics, NIMH, Bldg. 36, Rm			
	3006, MSC 4094, Bethesda, MD 20892-4094, USA			
	Location/Qualifiers			

CD5

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GABA-B receptor encoded by Genbank Accession Number
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polyA-signal  
polyA-site  
BASE COUNT 1334 a 1603 c 1395 g 1120 t 7 others  
ORIGIN

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RESULT	10
LOCUS	Af074482
DEFINITION	Rattus norvegicus GABA-B receptor 2 (GABA-Br2) mRNA, complete cds.
ACCESSION	Af074482
VERSION	Af074482.1
KEYWORDS	GI:4107510
SOURCE	Norway rat.
ORGANISM	Rattus norvegicus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
AUTHORS	1 (bases 1 to 2823) Jones,K.A., Broowsky,B., Tamm,J.A., Craigs,D.A., Durkin,M.M., Dal,M., Yao,W.-J., Johnson,M., Gunwaldsen,C., Huang,L.-Y., Tang,C., Shen,Q., Salton,J.J., Morse,K., Laz,T., Smith,K.E., Nagathnam,D., Noble,S.A., Branchek,T.A. and Gerald.C. GABA(B) receptors function as a heteromeric assembly of the subunits GABA(B)R1 and GABA(B)R2 Nature 396 (6712), 674-679 (1998)
TITLE	2 (bases 1 to 2823) Broowsky,B., Laz,T. and Gerald.C. Direct Submission
JOURNAL	Submitted (25-JUN-1998) Department of Molecular Biology, Synaptic Pharmacological Corporation, 215 College Road, Paramus, NY 07652, USA
MEDLINE	3 (bases 1 to 2823) Broowsky,B., Laz,T. and Gerald.C. Direct Submission
REFERENCE	Submitted (06-JAN-1999) Department of Molecular Biology, Synaptic Pharmaceutical Corporation, 215 College Road, Paramus, NY 07652, USA
AUTHORS	
TITLE	
JOURNAL	
REMARK	Sequence update by submitter
COMMENT	On Jan 7, 1999 this sequence version replaced gi:4038341.
FEATURES	Location/Qualifiers
SOURCE	1..2823 /organism="Rattus norvegicus" /db_xref="taxon:10116" /tissue_type="hypothalamus" 1..2823 /gene="GABA-Br2" 1..2823 /note="G protein-coupled receptor" /codon_start=1 /product="GABA-B receptor 2" /protein_id="AAD0335.1" /db_xref="GI:4038342"
gene	/translation="MASPSSSGQPPPPPAPKLLPILLSILLMLWAPAGMGWTRGAPRPSSPLSLGLMPLELKEVAKGSIGRWLPAAVELAIQINESLRLPYFDLRPYADPCDDNKGKAFKYDAIKYGPNHLMWGVCPSVTSLIASLGMNLVOLSFATIRVLARKKKYPFRFYSDBNAVPALIKTLKHFRRRAVLTLDODRFSEVNSMTDITGVLYGEDEIDTSESNDPCTSVKRLKGNVRLIIFOPDNMAKYFCCAFESBMSGSKXOWIIHWGPWEPAWEOHYEANSRCRLSRLLAAMEGTICVDPEFLSRQITTSKTPQQREYENSKRSYGPKSFHGIVAYDIGLVIAKTQLQRAETLHASRQRIDPFYTHPTLGLTILLANMETNEFGVTQGVVRNGRMGITIKFTOFDEREVKGVSNVAADTLERINDIRFOGESNPDKTIILPOLRKISLPISTLILMIASAFEPNIKRNKO KLIMKSPYNNLIILGLMLSYASFELGDSVSSETTELCITVRMITLVGTAAEGAEAKTWRAHALFNKNMKKKLIKOKKLVIYGMMLDICITLQMCAANDPRRVRYEMEPDRAGRDISTIRPLEHCENTHTITLGLTVAYKGLMLFGCLAMETNVSSIPALNDSKITGRSVANGIMCIIIGAASFLTDQNVOCIALVLIIFCSITTCCLAVPVFKLITLRPDAAQNORRFQTOQNKEDSKTSYSVNQASTSLRGQSSEHHRLRMKILTEDKDLEVMLOADRFEKTYIKQNTYICLNIDILSGNFESTDGKAILKHKKLDONQOLQMTTESRCKDIIEDINSSEHIHQRLSLQPLILHAYLPSIGVASCVSPCVSPASPRHRHVPPSFRMVSGGL"
CDS	

BASE COUNT      677 A      857 C      741 G      548 T

ORIGIN

Query Match      68.4%;    Score 2218.2;    DB 12;    Length 2823;

Best Local Similarity    89.6%;    Pred. No. 0;

Matches 2385;    Conservative 0;    Mismatches 278;    Indels 0;    Gaps 0;

QY	277	CGCTCTCATATGAGGCTCATGCGCTCATCCACCAAGAGGTGGCCAGAGGCTACATCGG	336
Db	160	CGGCTCTCATATGAGGCTCATGCGCTCATCCACCAAGAGGTGGCCAGAGGCTACATCGG	219
QY	337	CGGGGTGCTCCCGCGGTGAAGTGGCCATTCAGAGCATTCGCAACGATGATCTC	396
Db	220	CGGGGTGCTCCCGCGGTGAGTGAACATTCAGAGCATTCGCAACGATGATCTC	279
QY	397	CGGCTTACTTCTCGACCTCGGCTTATGACACGGAGTGGCAACGCAAAAGGTTG	456
Db	280	CGGCTTACTTCTCGACCTCGGCTTATGACACGGAGTGGCAACGCAAAAGGTTG	339
QY	457	AAAGCCTTACGATGCGATTAATTAAGGGCCGAACCACTGATGGTGTGGAGGCTC	516
Db	340	AAAGCCTTACGATGCGATTAATTAAGGGCCGAACCACTGATGGTGTGGAGGCTC	399
QY	517	TGTCATCGCTCACATCCATATTGACAGAGTCCCTCCAAAGGCTGGAATCTGTGACGTT	576
Db	400	TGTCGCTGCTCATCTATTATTCGGGAGTCCCTCCAAAGGCTGGAATCTGTGACGTT	459
QY	577	TGTTTTGCTGCACACAGCCCTGTTCTAGCGATTAAGAAAAATACCTTATTTTCTTGG	636
Db	460	TGTTTTGCTGCACACAGCCCTGTTCTAGCGATTAAGAAAAATACCTTATTTTCTTGG	519
QY	637	ACCGTCCCATCAGACAAATGCGGTAATCCAGCCATTGTGAAGTGTGCTCAAGCACTCCAG	696
Db	520	ACGGTCCCATCAGACAAAGCGGGTAAACCCCGCATCTGTGAAGCTCTGAAAGCACTTCCG	579
QY	697	TGGAAAGCCGCTGGGACGCTTACGCCAAGAGCTTACAGAGTCTGTAGAGTGGCGAATGAC	756
Db	580	TGGCGGCTGTGGGACACTCCACGACGAGCTGACAGCGCTTCCAGAGGTGAGAGATGAC	639
QY	757	CTGACTGGAGTTCTGTAGGGGAGGACATTGAGTTTCAACACCGAGAGCTTCTCACC	816
Db	640	CTGACTGGAGTTCTGTATGGGAGATATTGAGTTCTCAACACGAGAGTTTCTCACC	699
QY	817	GATCCCTTACCAAGTGTCAAAAAGCTCAAGGGGAATGATGTGCGATTCATCTTGGCCAG	876
Db	700	GATCCCTTACCAAGCTGTCAAAAAGCTCAAGGGGAATGATGCTGGGATTCATCTTGGCCAG	759
QY	877	TTTGCACGAAATATGGGACGAAAGTCTCTGTTGTGCATACGAGGAGAACTATGTGT	936
Db	760	TTTGCACGAAATATGGGACGAAAGTCTCTGTTGTGCCTTCAGAGGAGCAATGTTTGGC	819
QY	937	AGTAATATCAAGTGATTCATTCGCGGCTGTGTACGAGCCCTTGTGTGGAGAGAGGTGCAC	996
Db	820	AGCAATGACAGTGTGATCATCCCGGATGGTTAGAGAGCTTCGTTGGGAGCAGGTGCAT	879
QY	997	ACGGAAGCCACTATCCCGCTGCTTCGGAAGAAATCTGCTTGCCTCAATGAGGGCTAC	1055
Db	880	GTGGAGGCAATTCCTCAAGCTGTGCTGCGGAGAAAGCTCTGTGCTCCATGAGAGGTTAC	939
QY	1057	ATTGCGTGTGATTCGAGAGCCCTAGTGTCCACAGATCAAGACATTCACAGAAAGAT	1111
Db	940	ATTGCGAGTGTGAGAGCCCTAGTGTCCCAACAATCAAGCACTTCACAGAGGAT	999
QY	1117	CCACAGCAGTATGAGAGAGATACACACACAGCGGTCAAGGCGTGGGCGCCACGAAATT	1176
Db	1000	CCACAGCAGTATGAGAAAGAGTACACACAGCAACGTTACAGGCGTGGGCGCCACGAAATT	1055
QY	1177	CACGGGTACGCTCAATGACATCTGGGTCAATGCCAABACACTGCAAGAGGCTATGGAG	1233
Db	1060	CATGGGTACGCTCAATGAGATCTGGGTATGCCAABACCTTACAGAGGCTATGGAG	1111
QY	1237	ACACTGATGCAACACCGGACACAGCGGATCAGAGATTCAATACACGAGACACAG	1299
Db	1120	ACACTGATGCAAGTACAGAGCAACAGCGGATCAGAGATTCAATACACACACACAG	1179
QY	1297	CTGGGCAAGATCACTCTCAATGCCATGAAACAGAGACCACTTCTTGGGGCTACGGGTCAA	1355
Db	1180	CTGGGCAAAATCACTCTCAATGGCATGAAAGACACCACTTCTTGGGGCTACGGGTCAA	1233
QY	1357	GTATATCCGGAATGGGAGAAATAGGGGACATTAAATTACCAATTTCAACAGC	1416

Db 1240 GTTGTGTTCCGGAAAGGGGAGAGATGGAGACATTAATTACTCAATTCAGACAGC 1299  
Qy 1417 AGGAGGTGAAGGTGGAGAGTACACGCTGTGGCCGACACACTGGAGATCATTAAGAC 1476  
Db 1300 AGAGAGGTGAAGGTGGAGATACACGCGGTGGCTGACACACTGGAGATCATTAAGAC 1359  
Qy 1477 ACCATCAGATTCACAGATTCGAGAACCAACAAAGACATCATCTGTGGAGCAGCTG 1536  
Db 1360 ACCATCAGATTCACAGAGGTTCGAGAGGTCCGAGCCACCAAGACATCATCTGTGGAGCAGCTT 1419  
Qy 1537 CGGAAGATCTCCCTACCTCTCTACAGATCCCTCTGCCCCACCATCTGGAGATGATC 1596  
Db 1420 CGGAAGATCTCCCTCTCACTGATAGCATCTCTGCTCCCTCTACCATCTCCGATGATC 1479  
Qy 1597 ATGGCCACTGCTTTCTCTCTTCTTCAACATCAAGAACCCGATCAGAGCTCATTAAGTG 1656  
Db 1480 ATGGCCAGCGCTCTCTCTCTTCAACATCAAGAACCCGATCAGATTAAGATG 1539  
Qy 1657 TCGAGTCCATACATGACACACCTTATCATCTTGGAGGAGTCTTCTCTATGCTTCATA 1716  
Db 1540 TCAACCCCTACATTAACACCTCTCATCTCTGGAGAGATGCTGTCTATGATCATC 1599  
Qy 1717 TTTCTCTTGGCCCTGATGATGATCTCTTGTCTGAAAAAGCCTTGAACACTTTGCACC 1776  
Db 1600 TTCTCTTTGGCCCTGATGATGATCTCTTGTCTGAAAAAGCCTTGAACACTTTGCACC 1659  
Qy 1777 GTGAGAGCTGATCTCAACCTGGGGCTACACAGACGCTTTTGGGGCCATGTTTGAAG 1836  
Db 1660 GTCCGAGCTGATCTCAACCTGGGGCTACACAGACGCTTTTGGGGCCATGTTTGAAG 1719  
Qy 1837 ACCTGAGAGTCCACGACCTTCTCAAAATGTAAATGAAGAAAGATCATCAAGAC 1896  
Db 1720 ACCTGAGAGTCCACATGCTCTTCAAAATGTAAATGAAGAAAGATCATCAAGAC 1779  
Qy 1897 CAGAAACTGCTTGTGATCGTGGGGGCGATGCTGTGATGACCTGTATCTGATCTGC 1956  
Db 1780 CAGAACTGCTTGTGATCGTGGGGGCGATGCTGTGATGACCTGTGATCTGATCTGT 1839  
Qy 1957 TGGCAGGCTGTGAGACCCCTCGGAAAGACAGTGGAGATGAGATGGAGCCGAGACCA 2016  
Db 1840 TGGCAGGCTGTGAGACCCCTCGGAGAGACAGTGGAGATGAGATGGAGCCGAGACCA 1899  
Qy 2017 GCAGAGCGGAGATATCATCCGCCCTCTCTGAGACACTGTGAGAACCCCATATGACC 2076  
Db 1900 GCAGCGCCGGAGATATCATCCGCCCATGTGCGAACAATGGGAAAAACCCACATGACC 1959  
Qy 2077 ATCTGCTTGGCATGCTCTATGCTTCAAGAGACTTCTATGTTGCTGCTGTTCTTA 2136  
Db 1960 ATCTGCTTGGCATGCTCTATGCTTCAAGAGGCTCTCTATGCTGCTGTTCTTCTTG 2019  
Qy 2137 GCTTGGGAGACCCGAGACGACATCCCGGACACTCAAGACAGACAGTACATGGAGT 2196  
Db 2020 GCATGGGAAACCCGAGATGAGACATCCCTGACCTCAAGACAGACAGTACATGGAGT 2079  
Qy 2197 AGTGTCTAACCTGGGAGTATGATGATCATGAGGGCGCTGTCTCTCTGACCCGG 2256  
Db 2080 AGTGTCTAACATGTGGGAGTATGATGATCATGAGGGCGCTGTCTCTCTGACCGCT 2139  
Qy 2257 GACCAAGCCATATGAGATTTCTGATCGTGGCTGTGATCATCTTCTGACAGCATC 2316  
Db 2140 GACCAAGCCATATGAGATTTCTGATCGTGGCGCTGTGATCATCTTCTGACAGCATC 2199  
Qy 2317 ACCCTGCTGCTGATCTGATCTGAGAGCTCATCACCTGAGCAAAACCATGACAGCA 2376  
Db 2200 ACTCTGCTGCTGATCTGATCTGAGAGCTCATCTCTGAGCAAAACCATGACAGCGC 2259  
Qy 2377 ACCGAGAAACGGGATTCAGATTCATCTCAGAAATCAGAGAAAGAGATTCATAAAGCTCC 2436  
Db 2260 ACCGAGAAACGGGATTCAGATTCATCTCAGAAACAGAAAGAGATTCATAAAGCTCC 2319  
Qy 2437 ACCTGCTGACCAAGTGTGAACCAAGCAGACATCCCGCTGAGAGGCGCTACAGTACAGAA 2496

Db 2320 ACTTCAGTCACAGCGGTGAACAGGCGAGACAGCTCAACCTCTGGAGGAGCTGACATCAGAA 2379  
Qy 2497 AACCATCGCCTGGGAATGAAGATCAGACAGCTGATTAAGACTTGGAGAGCTCACCATG 2556  
Db 2380 AACCATCGCCTTGAATGAAGATCAGACAGCTGAGCAAAAGACTTGGAGAGCTCACCATG 2439  
Qy 2557 CAGCTCAGAGACACACAGAAAAAGACACCTTAACTTAAACAGACACCTACCAAGACTC 2616  
Db 2440 CAGCTCAGAGACACACAGAAAAAGACACCTTAACTTAAACAGACACCTACCAAGACTC 2499  
Qy 2617 AATGATCTCTCAACCTGGGAAACTTCACTGAGAGACAGATGAGGAAAGGCAATTTTA 2676  
Db 2500 AAGACATCTCTGCTTGGGCACTTCAAGAGAGACAGATGAGGAAAGGCAATTTTA 2559  
Qy 2677 AAAATACCTCGATCAAAATCCCAAGCTACAGTGGAGACAAACAGAGCCCTCTGAGAA 2736  
Db 2560 AAAATACCTCGATCAAAATCCCAAGCTACAGTGGAGACAAACAGAGCCCTCTGAGAA 2619  
Qy 2737 TGCAGATCTCTTATAGAGATTAATCTCCAGAAACATCCAGCTGCTGCTCCCTC 2796  
Db 2620 TGCAGAGACCCATAGAGATCACTCCCGAGACATCCAGCTGCTGCTCCCTC 2679  
Qy 2797 CAGCTCCCATCTCTCCAGACAGCTACCTCCATCCATCCATCCAGAGGCGTGGAGCCAGCTGT 2856  
Db 2680 CAGCTCCCATCTCTCCAGACAGCTACCTCCATCCATCCATCCAGAGGCGTGGAGCCAGCTGT 2739  
Qy 2857 GTGAGCCCTGCTGCTGAGCCCAAGCCGAGCCGCGGACAGATGTGCCACCTCTTC 2916  
Db 2740 GTGAGCCCTGCTGCTGAGCCCAAGCCGAGCCGCGGACAGATGTGCCACCTCTTC 2799  
Qy 2917 CGAGTCAATGCTTGGGCTCTGA 2939  
Db 2800 CGAGTCAATGCTTGGGCTCTGA 2822

RESULT 11  
AF095723 743 bp mRNA PRI 08-OCT-1998  
LOCUS AF095723 Homo sapiens GABA-B receptor splice variant 1 mRNA, partial cds.  
DEFINITION AF095723  
ACCESSION AF095723  
VERSION AF095723.1 GI:3719471  
KEYWORDS human.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 743)  
AUTHORS Clark,J.C., Lam,A. and Bonner,T.I.  
TITLE gB2, a second GABA-B receptor  
JOURNAL Unpublished  
2 (bases 1 to 743)  
AUTHORS Clark,J.C., Lam,A. and Bonner,T.I.  
TITLE Direct Submission  
JOURNAL Mental Health, Bldg 36, Rm 3D06, MSC 4094, Bethesda, MD 20892-4090,  
USA

FEATURES  
source Location/Qualifiers  
1..743  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/tissue\_type="brain"  
/map="D9S287-D9S176"  
/chromosome="9"  
<1..549  
/note="alternative splice variant of GABA-B receptor  
encoded by GenBank Accession Number AF056085; G  
protein-coupled receptor; gB2"  
/codon\_start=1  
/product="GABA-B receptor splice variant 1"  
/protein\_id="A063383.1"  
/db\_xref="GI:3719472"  
/translation="ITLCLVFPKLTLLRPNPDAATONRRFOFTONOKKEDSKTSY  
TSVNAQSTSRLEGLQSENHRLRMKITELDLDEYVMQADPPEKTTYIKONHYELN

DIINLGNFESTIDGKAILKNHLDONPOLQWNTBPSRTCKPIEDINSPIHQRRIS  
 LQPLIHHRVPPSPFRVWVSGT  
 BASE COUNT 214 a 225 c 181 g 123 t  
 ORIGIN

Query Match 20.2%; Score 655; DB 11; Length 743;  
 Best Local Similarity 90.5%; Pred. No. 4.8e-127;  
 Matches 743; Conservative 0; Mismatches 0; Indels 78; Gaps 1;

QY 2314 ATCAACCCCTGCTGTGATTCGTCGCCAAGCTCATCCCTGAGAACAAACCCAGATGCA 2373  
 DB 1 ATCAACCCCTGCTGTGATTCGTCGCCAAGCTCATCCCTGAGAACAAACCCAGATGCA 60  
 QY 2374 GCAACGCAAGAGGCGGATTCAGTCTACCTAGATCAGAGAGAGAGATTTCTAAACG 2433  
 DB 61 GCAACGCAAGAGGCGGATTCAGTCTACCTAGATCAGAGAGAGAGATTTCTAAACG 120  
 QY 2434 TCCACCTGCTGACAGGTGTAACCAAGCCAGCATCCCGCTGGAGGGCTACAGTCA 2493  
 DB 121 TCCACCTGCTGACAGGTGTAACCAAGCCAGCATCCCGCTGGAGGGCTACAGTCA 180  
 QY 2494 GAAACCATGCTGCTGCAATGATCAGAGAGCTGGATTAAGACTTGAAGAGTCCACC 2553  
 DB 181 GAAACCATGCTGCTGCAATGATCAGAGAGCTGGATTAAGACTTGAAGAGTCCACC 240  
 QY 2554 ATGCAAGCTGCAAGAGACCAAGCAACCACTACATTTAAAGAACCACTACCAAGAG 2613  
 DB 241 ATGCAAGCTGCAAGAGACCAAGCAACCACTACATTTAAAGAACCACTACCAAGAG 300  
 QY 2614 CTCAATGACATCTCAACCTGGAACCTGAGAGACAGATGGAGGAAAGCCATT 2673  
 DB 301 CTCAATGACATCTCAACCTGGAACCTGAGAGACAGATGGAGGAAAGCCATT 360  
 QY 2674 TTTAAATAATCCTGATGATCAAAATCCCGAGCTAGAGTGAACACACAGAGCCCTTCA 2733  
 DB 361 TTTAAATAATCCTGATGATGATCAAAATCCCGAGCTAGAGTGAACACACAGAGCCCTTCA 420  
 QY 2734 ACATGCAAGATCTATATGAGATATATACTCTCAGAACATCAAGCTGCGCTGTCC 2793  
 DB 421 ACATGCAAGATCTATATGAGATATATACTCTCAGAACATCAAGCTGCGCTGTCC 480  
 QY 2794 CTCAAGCTGCTGATCTGACACAGCCTACCTCCATCATCGAGAGGCTGAGGCCAGC 2853  
 DB 481 CTCAAGCTGCTGATCTGACACAGCCTACCTCCATCATCGAGAGGCTGAGGCCAGC 501  
 QY 2854 TGTGTCAAGCCCTGGGTGAGCCACGCCAGCCCGCCGACAGACATGTCACACCTCC 2913  
 DB 501 TGTGTCAAGCCCTGGGTGAGCCACGCCAGCCCGCCGACAGACATGTCACACCTCC 522  
 QY 2914 TTCCGATGATGCTGTGCGGCTGTAAAGGTGGAGGCTGGGCGCCCTGCCCGCT 2973  
 DB 523 TTCCGATGATGCTGTGCGGCTGTAAAGGTGGAGGCTGGGCGCCCTGCCCGCT 582  
 QY 2974 GACAGAACCACTAGTGGGAGAGGGGCTGCTGCTGAGAACCACTGCGGCTGTGCTGCGA 3033  
 DB 583 GACAGAACCACTAGTGGGAGAGGGGCTGCTGCTGAGAACCACTGCGGCTGTGCTGCGA 642  
 QY 3034 GAAAGCTGGACCACTGCTGCTGCTGCTGAGAACCACTGAGTGGACACTCAGGTGGAGAG 3093  
 DB 643 GAAAGCTGGACCACTGCTGCTGCTGCTGAGAACCACTGAGTGGACACTCAGGTGGAGAG 702  
 QY 3094 CGGGGACAGGGGAGAGACTGAGCACTGACCTGACCTTATT 3134  
 DB 703 CGGGGACAGGGGAGAGACTGAGCACTGACCTGACCTTATT 743

RESULT 12  
 AF095724 740 bp mRNA PRI 08-OCT-1998  
 LOCUS  
 DEFINITION Homo sapiens GABA-B receptor splice variant 2 mRNA, partial cds.  
 ACCESSION AF095724  
 VERSION AF095724.1 GI:3719473

# KEYWORDS

SOURCE  
 ORGANISM

human.  
 Homo sapiens

## REFERENCE

1 (bases 1 to 740)  
 Clarke, J.C., Lam, A., and Bonner, T.I.  
 9b2, a second GABA-B receptor  
 Unpublished  
 2 (bases 1 to 740)  
 Clarke, J.C., Lam, A., and Bonner, T.I.  
 Direct Submission  
 Submitted (27-MAR-1998) Section on Genetics, National Institute of  
 Mental Health, Bldg 36, Rm 3D06, MSC 4094, Bethesda, MD 20892-4090,  
 USA

## FEATURES

source

Location/Qualifiers  
 1..740  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /tissue\_type="brain"  
 /map="D9S287-D9S176"  
 /chromosome="9"

## CDS

/note="alternative splice variant of GABA-B receptor  
 encoded by Genbank Accession Number AF056085; G  
 protein-coupled receptor; 9b2"  
 /product="GABA-B receptor splice variant 2"  
 /protein\_id="AAC6384.1"  
 /db\_xref="GI:3719474"

## BASE COUNT

215 a 235 c 172 g 118 t

Query Match 20.0%; Score 649; DB 11; Length 740;  
 Best Local Similarity 90.1%; Pred. No. 8.7e-126;  
 Matches 740; Conservative 0; Mismatches 0; Indels 81; Gaps 1;

QY 2314 ATCAACCCCTGCTGTGATTCGTCGCCAAGCTCATCCCTGAGAACAAACCCAGATGCA 2373  
 DB 1 ATCAACCCCTGCTGTGATTCGTCGCCAAGCTCATCCCTGAGAACAAACCCAGATGCA 60  
 QY 2374 GCAACGCAAGAGGCGGATTCAGTCTACCTAGATCAGAGAGAGAGATTTCTAAACG 2433  
 DB 61 GCAACGCAAGAGGCGGATTCAGTCTACCTAGATCAGAGAGAGAGATTTCTAAACG 120  
 QY 2434 TCCACCTGCTGACAGGTGTAACCAAGCCAGCATCCCGCTGGAGGGCTACAGTCA 2493  
 DB 121 TCCACCTGCTGACAGGTGTAACCAAGCCAGCATCCCGCTGGAGGGCTACAGTCA 180  
 QY 2494 GAAACCATGCTGCTGCAATGATCAGAGAGCTGGATTAAGACTTGAAGAGTCCACC 2553  
 DB 181 GAAACCATGCTGCTGCAATGATCAGAGAGCTGGATTAAGACTTGAAGAGTCCACC 240  
 QY 2554 ATGCAAGCTGCAAGAGACCAAGCAACCACTACATTTAAAGAACCACTACCAAGAG 2613  
 DB 241 ATGCAAGCTGCAAGAGACCAAGCAACCACTACATTTAAAGAACCACTACCAAGAG 300  
 QY 2614 CTCAATGACATCTCAACCTGGAACCTGAGAGCAAGATGGAGGAAAGCCATT 2673  
 DB 301 CTCAATGACATCTCAACCTGGAACCTGAGAGCAAGATGGAGGAAAGCCATT 360  
 QY 2674 TTTAAATAATCCTGATGATGATCAAAATCCCGAGCTAGAGTGAACACACAGAGCCCTTCA 2733  
 DB 361 TTTAAATAATCCTGATGATGATCAAAATCCCGAGCTAGAGTGAACACACAGAGCCCTTCA 420  
 QY 2734 ACATGCAAGATCTATATGAGATATATACTCTCAGAACATCAAGCTGCGCTGTCC 2793

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Db      421 ACATGCAAGATCTTAGAGATATTAACCTCTCCAGAACATCCAGCTGGCTGCC 480
Qy      2794 CTCACAGTCCCATCTCCACACGCTACCTCCATCCATCGAGGGGTGGAGCCAGC 2853
Db      481 CTCACAGTCCCATCTCCACACGCTACCTCCATCCATCGAGGGGTGGAGCCAGC 540
Qy      2854 TGTGTACGCCCCCTGGGTACAGCCCCACGCGCAGCCCCGGCACAGCATGTGCCACCTCC 2913
Db      541 TGTGTACGCCCCCTGGGTACAGCCCCACGCGCAGCCCCGGCACAGCATGTGCCACCTCC 581
Qy      2914 TTCGAGATCATGTCTCGGGGCTGTAAAGGTGGAGAGGCTGGGGCCCGGGGCTCCCGCT 2973
Db      581 ----- 581
Qy      2974 GACAGAACACACATGGGCGAGAGGGGTCTGCTGCAGAAACATGTCGGCTTGGCTGCCGA 3033
Db      581 -ACAGAACACACATGGGCGAGAGGGGTCTGCTGCAGAAACATGTCGGCTTGGCTGCCGA 639
Qy      3034 GAAGCTGGGCGACCATGGCTGGCTCTCAGAGACCATCGGATGGCATCAGTGGACAGGA 3093
Db      640 GAAGCTGGGCGACCATGGCTGGCTCTCAGAGACCATCGGATGGCATCAGTGGACAGGA 699
Qy      3094 CGGGCGAGGGGAGAGACTTGGACACTGACCTCGAGCCTTATT 3134
Db      700 CGGGCGAGGGGAGAGACTTGGACACTGACCTCGAGCCTTATT 740

```

## RESULT 13

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LOCUS      AB015334      465 bp      mRNA      PRI      06-FEB-1999
DEFINITION Homo sapiens HRIHFB2099 mRNA, partial cds.
ACCESSION  AB015334
VERSION     AB015334.1 GI:3970857
KEYWORDS    HRIHFB2099.
SOURCE      Homo sapiens fetus brain cDNA to mRNA.
ORGANISM    Homo sapiens Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Eukaryota; Catarrhini; Homiidae; Homo.

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REFERENCE   1 (bases 1 to 465)
AUTHORS     Ueki,N.
TITLE       Direct Submission
JOURNAL     Submitted (08-JUN-1998) to the DDBJ/EMBL/GenBank databases.
            Nobuhide Ueki, Helix Research Institute, Inc., Biological
            Technology Lab., 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            (E-mail:ueki@hri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952)

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REFERENCE   2 (sites)
AUTHORS     Ueki,N., Oda,T., Kondo,M., Yano,K., Noguchi,T. and Muramatsu,M.A.
TITLE       Selection system for genes encoding nuclear-targeted proteins
JOURNAL     Nature Biotech. 16, 1338-1342 (1998)
FEATURES
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                1..465
                    /organism="Homo sapiens"
                    /db_xref="taxon:9606"
                    /dev_stage="fetus"
                    /tissue_type="brain"
                    1..372
                    /gene="HRIHFB2099"
                    <1..372
                    /gene="HRIHFB2099"
                    /codon_start=1
                    /protein_id="BA34793.1"
                    /db_xref="GI:3970858"
                    /translation="DAMASVCGPSSSPSTPTSHPSSEAMTPAVSAPASAPPAPATD
                    MCHPSESWSRACKGRPGPGASPTPEPHMAGSAAETLSALAAKLTGMGLSGPLG
                    WHSGGDGAGDLPADLPLEYL"

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BASE COUNT      92 a      152 c      138 g      83 t
ORIGIN

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Query Match      14.0%; Score 454; DB 9; Length 465;
Best Local Similarity 100.0%; Pred. No. 4.8e-85;
Matches 454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      2778 CCAAGCTGGCTGCTCCCTCCAGCTCCCACTCCCAACACGCTTACTCCATCCATCGG 2837
Db      11 CCAAGCTGGCTGCTCCCTCCAGCTCCCACTCCCAACACGCTTACTCCATCCATCGG 70
Qy      2838 AGGGGTGAGCGCCAGCTGTGTACAGCCCTGCGTCACGCCACCGCCAGCGCCGACAG 2897
Db      71 AGGGGTGAGCGCCAGCTGTGTACAGCCCTGCGTCACGCCACCGCCAGCGCCGACAG 130
Qy      2898 ACATGTGCCACCTCTCTCCGAGTCATGTGTCTGGGCTGTAAAGGTGGAGAGGCTGGGC 2957
Db      131 ACATGTGCCACCTCTCTCCGAGTCATGTGTCTGGGCTGTAAAGGTGGAGAGGCTGGGC 190
Qy      2958 CCGGGGCTCTCCCGGTACAGAACACACACTGGGCGAAGGGGTGTGTGAGAAACACTGT 3017
Db      191 CCGGGGCTCTCCCGGTACAGAACACACACTGGGCGAAGGGGTGTGTGAGAAACACTGT 250
Qy      3018 CGGCTGTGGCTGGGAGAACACTGGGCGACATGGCTGGCTCTCAGAGACCATCGATGGC 3077
Db      251 CGGCTGTGGCTGGGAGAACACTGGGCGACATGGCTGGCTCTCAGAGACCATCGATGGC 310
Qy      3078 ACTAGGTGGACAGAGAGAGGGGAGAGCTTGGACCTGACCTGAGACCTTATTGT 3137
Db      311 ACTAGGTGGACAGAGAGAGGGGAGAGCTTGGACCTGACCTGAGACCTTATTGT 370
Qy      3138 GAATCTCTATTCTTCTTCAAAAGAGAGAAAGGAATGGAGCTCTCTTAAACATCTG 3197
Db      371 GAATCTCTATTCTTCTTCAAAAGAGAGAAAGGAATGGAGCTCTCTTAAACATCTG 430
Qy      3198 CAACCAAGAGAGGCGCTGGATATCAAACTTGCA 3231
Db      431 CAACCAAGAGAGGCGCTGGATATCAAACTTGCA 464

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## RESULT 14

```

LOCUS      AC011957      153790 bp      DNA      HTG      16-OCT-1999
DEFINITION Homo sapiens chromosome 9 clone 199_C_17 map 9, *** SEQUENCING IN
            PROGRESS ***, 11 unordered pieces.
ACCESSION  AC011957
VERSION     AC011957.1 GI:6056224
KEYWORDS    HTG; HTGS_PHASE1.
SOURCE      human.
ORGANISM    Homo sapiens Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eukaryota; Primates; Catarrhini; Homiidae; Homo.

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REFERENCE   1 (bases 1 to 153790)
AUTHORS     Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
            Baldwin,D., Barna,N., Beckerly,R., Boguslavsky,L., Boukhgalter,B.,
            Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
            Cooke,P., Dearlano,K., Dewar,K., Domono,M., Donegan,L., Doyle,M.,
            Ferreira,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D., Horton,L.,
            Galagan,J., Gardina,S., Grant,G., Hagos,B., Heathford,A., Horton,L.,
            Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
            Lehoccky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
            McEwan,P., McGuck,A., McKernan,K., McLaughlin,J., Meldrum,J.,
            Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
            Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
            Stenge-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
            Testaye,S., Tittrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
            Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.

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TITLE       Direct Submission
JOURNAL     Submitted (16-OCT-1999) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
            All repeats were identified using RepeatMasker: Smit, A.F.A. &
            Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html.

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* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is

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\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
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\* gap of unknown length  
\* 3490 7448: contig of 3959 bp in length  
\* gap of unknown length  
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\* gap of unknown length  
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Db 104963 CGGAGGCTGGAGCCGACAGCTGTTCAGGCCCTGGCTGACGCCCGACGCCGCCGCCA 105022  
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|||||  
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LOCUS  
DEFINITION  
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mRNA, complete cds.  
AF145639  
VERSION  
AF145639.1 GI:5052567  
KEYWORDS  
fruit fly.  
SOURCE  
ORGANISM  
Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
REFERENCE  
1 (bases 1 to 3989)  
Rubin,G.M., Wan,K.H., Harvey,D., Lewis,S.E., Brokstein,P.,  
Tsang,G., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,  
Butenhoff,C., Champe,M., Chavez,C., Chew,M., Doyle,C.M.,  
Farfan,D.E., Friese,E., Galle,R., George,R.A., Harris,N.L.,  
Hoskins,R.A., Evans-Holm,M., Houston,K.A., Hummatti,S.R., Kim,E.,  
Li,P., Moshrefi,M., Pacled,J.M., Park,S., Sequeira,A., Sethi,H.,  
Snir,E., Svitskas,R.R., Weinburg,T. and Celniker,S.E.  
Full length Drosophila melanogaster cDNA sequence  
Unpublished  
2 (bases 1 to 3989)  
Rubin,G.M., Wan,K.H., Harvey,D., Lewis,S.E., Brokstein,P.,  
Tsang,G., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,  
Butenhoff,C., Champe,M., Chavez,C., Chew,M., Doyle,C.M.,  
Farfan,D.E., Friese,E., Galle,R., George,R.A., Harris,N.L.,  
Hoskins,R.A., Evans-Holm,M., Houston,K.A., Hummatti,S.R., Kim,E.,  
Li,P., Moshrefi,M., Pacled,J.M., Park,S., Sequeira,A., Sethi,H.,  
Snir,E., Svitskas,R.R., Weinburg,T. and Celniker,S.E.  
Direct Submission  
Submitted (23-APR-1999) Berkeley Drosophila Genome Project,  
University of California Berkeley, Berkeley, CA 94720, USA  
For further information about this sequence, including its location  
and relationship to other sequences, please visit our web site  
(http://fruitfly.berkeley.edu) or send email to  
cdna@fruitfly.berkeley.edu.  
Location/Qualifiers  
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Tue Mar 21 10:26:18 2000

us-09-211-755-1.rge

Page 24

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GenCore version 4.5  
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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C 1	46.2	1.4	7218	1	US-08-232-463-14	Sequence 14, Appl
2	45.4	1.4	2176	7	5320958-1	Patent No. 5320958
3	43.8	1.4	4095	6	PCT-US91-09422-18	Sequence 18, Appl
4	43.8	1.4	2426	6	PCT-US91-09422-20	Sequence 20, Appl
5	41.8	1.3	1312	1	US-08-205-506A-1	Sequence 1, Appl
6	41.8	1.3	1312	6	PCT-US94-02389-1	Sequence 1, Appl
7	41.6	1.3	8438	1	US-07-945-283-1	Sequence 1, Appl
8	41.6	1.3	2823	1	US-08-398-008A-1	Sequence 1, Appl
9	41.6	1.3	2823	4	US-08-893-333-1	Sequence 1, Appl
C 10	40.6	1.3	10596	1	US-07-884-811-15	Sequence 15, Appl
C 11	40.6	1.3	10596	1	US-07-885-971-15	Sequence 15, Appl
C 12	40.6	1.3	10596	1	US-08-087-783A-15	Sequence 15, Appl
C 13	40.6	1.3	10596	3	US-08-194-088B-15	Sequence 15, Appl
C 14	40.6	1.3	10596	3	US-08-194-088B-15	Sequence 15, Appl
C 15	40.6	1.3	5452	4	US-09-130-114-1	Sequence 1, Appl
C 16	40.6	1.3	10596	6	PCT-US93-04648-15	Sequence 15, Appl
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20	40.4	1.2	1080	3	US-08-842-238-5	Sequence 5, Appl
21	40.4	1.2	1272	4	US-08-972-258-1	Sequence 1, Appl
C 22	39.8	1.2	15378	5	US-08-785-420-1	Sequence 1, Appl
C 23	39.2	1.2	3809	1	US-08-485-588-2	Sequence 3, Appl
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33	39.2	1.2	3809	5	US-08-353-784-3	Sequence 3, Appl
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43	38.2	1.2	1789	2	US-08-455-543A-3	Sequence 2, Appl
44	38.2	1.2	2338	2	US-08-455-543A-31	Sequence 31, Appl
45	38.2	1.2	5904	3	US-08-193-078B-3	Sequence 3, Appl

#### ALIGNMENTS

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RESULT 1
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
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GENERAL INFORMATION:
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APPLICANT: DORNER, F.
APPLICANT: SCHEFFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESS: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PTZgpt-Fls
US-08-232-463-14
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 Db 1413 RRR 1354  
 Oy 1199 TCTGGGTCATCGCCACAGACACTCAGAGGGCCATGAGACACTGCATGCCAGCAGCCGCG 1258  
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 Oy 1319 CCATGACGAGACCAACTCTTCTGGGGCTACGGGTCAAGTATATTCGGAGTGGGAGA 1378  
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 Oy 1379 GAATGGGACCATTAATTAATTCAATTTCACAGACGACGAGGTGAAGTGGGAGAGT 1438  
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 Db 1113 RR 1055  
 RESULT 2  
 3320958-1  
 Patent No. 5320958  
 APPLICANT: INOYE, SUNIKO; HSU, MEL-YIN; EAGLE, SUSAN;  
 INOYE, MASAYORI  
 TITLE OF INVENTION: ISOLATED BACTERIAL REVERSE TRANSCRIPTASE  
 NUMBER OF SEQUENCES: 24  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/315,316  
 FILING DATE: 24-FEB-1989  
 SEQ ID NO:1  
 LENGTH: 2176  
 3320958-1

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### RESULT 3

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PCT-US91-09422-18
; Sequence 18, Application PC/TUS9109422
; GENERAL INFORMATION:
; APPLICANT: Mulvihill, Eileen R.
; APPLICANT: Hagen, Frederick S.
; APPLICANT: Houmied, Khaled M.
; APPLICANT: Almers, Wolfhard M.
; TITLE OF INVENTION: G PROTEIN-COUPLED GLUTAMATE RECEPTORS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/09422
; FILING DATE: 19911212
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/672,007
; FILING DATE: 18-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/648,481
; FILING DATE: 30-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/626,806
; FILING DATE: 12-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-6PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4095 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: SN30
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 26..3198
PCT-US91-09422-18

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677 AGTTCCTAAGCACTACCAGTGGAGCGCGTGGGCACGCTGACCGAAGACG 727

Db 1094 ATATTGTCCGAGCCCTCAAGTGAACATATGTCTCACACTGGCCTCAGAGG 1144

## RESULT 4

PCT-US91-09422-20  
Sequence 20, Application PC/TUS9109422

## GENERAL INFORMATION:

APPLICANT: Mulvihill, Eileen R.  
APPLICANT: Hagen, Frederick S.  
APPLICANT: Houmed, Khaled M.  
APPLICANT: Almers, Wolfhard  
TITLE OF INVENTION: G PROTEIN-COUPLED GLUTAMATE RECEPTORS  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/09422  
FILING DATE: 19911212  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/672,007  
FILING DATE: 18-MAR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/648,481  
FILING DATE: 30-JAN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/626,806  
FILING DATE: 12-DEC-1990

## ATTORNEY/AGENT INFORMATION:

NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 13952-6PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 467-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2426 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: SR13

PCT-US91-09422-20

Query Match 1.4%; Score 43.8; DB 6; Length 2426;  
Best Local Similarity 49.4%; Pred. No. 0.083;

Matches 114; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

QY 497 TGATGTTGAGAGCGCTGTGCATCCGACATCCATCATGAGAGTCCCTCCAG 556  
Db 164 TGGGATCATGAGAGCTCGGGAGAGCTCGTCTGCATCATGAGAGTCCCTCCAG 223  
QY 557 GCTGATCTGAGAGCTTTCTTTGCTGACACCGCCCTGTTCTAGCCGATAGAAA 616  
Db 224 TCTTCAAGATCCCTGAGTACGATAGCTCCAGAGCCCTCGACTGAGTACACAGCC 283  
QY 617 AATACCTATTTCTTTGAGACCGTCCATCAGACAAATGGGTGATACAGCCATTGGA 676  
Db 284 GCTATGACTTCTTCTCCGCGGTGGTGGCTCAGACATACCAAGGCCAGGCGATGGTG 343

QY 677 AGTGTCTAAGACACTACAGTGAAGCGCGTGGGACCGCTGACGAGACG 727  
Db 344 ATATTGTCCGAGCCCTCAAGTGAACATATGTCTCACACTGGCCTCAGAGG 394

## RESULT 5

US-08-205-506A-1  
Sequence 1, Application US/08205506A  
Patent No. 5545563

## GENERAL INFORMATION:

APPLICANT: Darlington, Gretchen J.  
APPLICANT: Wilson, Deborah R.  
APPLICANT: Wilde, Margaret  
TITLE OF INVENTION: THE HUMAN C/EBP GENE AND VECTORS FOR  
NUMBER OF SEQUENCES: ITS EXPRESSION  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fulbright & Jaworski L.L.P.  
STREET: 801 Pennsylvania Avenue, NW  
CITY: Washington, D.C.  
STATE:  
COUNTRY: USA  
ZIP: 20004

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/205,506A  
FILING DATE: March 4, 1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Davis, Peter J.  
REGISTRATION NUMBER: 36,119  
REFERENCE/DOCKET NUMBER: 311,027  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 662-0200  
TELEFAX: (202) 662-4643  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1312 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: C/EBP

US-08-205-506A-1

Query Match 1.3%; Score 41.8; DB 1; Length 1312;  
Best Local Similarity 54.1%; Pred. No. 0.2;

Matches 85; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 2818 GCGTACCTCCATCCATCGAGAGCGGACGCGACAGTGTGACGCCCTGCGTACGCC 2877  
Db 797 GCCAGACACCATGACATCGACAGCGCCGACCCACAGCGCGCCGACAGCCGCGCA 856  
QY 2878 ACCGCCAGGCCCCGACAGAGATGTCACACCTCTCTCCAGTATGTCGCGGCTG 2937  
Db 857 GCCCGACCCCGCGCGCGCTCGGTGCGCGCGCGCTTCCGCGCCCTGCGAGCGGCTCA 916  
QY 2938 TAAGGTGGAGGCTCGAGCGCGGCGCTCCCGCG 2974  
Db 917 AGGGCTGGGCGCGCGACCCCGACTTCGCGCGAG 953

```
RESULT 6
PCT-US94-02389-1
; Sequence 1, Application PC/TUS9402389
; GENERAL INFORMATION:
; APPLICANT: Darlington, Gretchen J.
; APPLICANT: Wilson, Deborah R.
; APPLICANT: Wilde, Margaret
; TITLE OF INVENTION: THE HUMAN C/EBP GENE AND VECTORS FOR ITS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howrey & Simon
; STREET: 1299 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/02389
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Auerbach, Jeffrey I.
; REGISTRATION NUMBER: 32,680
; REFERENCE/DOCKET NUMBER: 225-107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 383-7451
; TELEFAX: (202) 383-6610
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1312 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: C/EBP
; PCT-US94-02389-1

Query Match 1.3%; Score 41.8; DB 6; Length 1312;
Best Local Similarity 54.1%; Pred. No. 0.2;
Matches 85; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 2818 GCCTACCTCCATCGAGGAGGCTGACGCCCTGCTGAGCCCTGCGTCAAGCCC 2877
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 797 GCGACGACCGACCTGACCTGACCGCCGCGGTCACCCGCGCGGCTGCGCCCA 856

QY 2878 ACCGCGACGCGCGCGACAGACATGTGCGACCCCTCCGAGTCATGCTCGGAGCCTG 2937
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 857 GCGCGACCGCGCGCGCGCTGCTGCGCGCGCGCTTCCGCGCCCTGACGAGCGCTCA 916

QY 2938 TAAGGTTGGAGGCTGCGCGCGCGGCGCTCCCGCGTG 2974
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 917 AGGGGCTGGCGCGCGACCGCGACCTCGCGCGAG 953

RESULT 7
US-07-945-283-1/c
; Sequence 1, Application US/07945283
; Patent No. 5352596
; GENERAL INFORMATION:
; APPLICANT: Cheung, Andrew K.
; APPLICANT: Wesley, Ronald D.
```

```
; TITLE OF INVENTION: Pseudorabies Virus Deletion Mutants
; TITLE OF INVENTION: Involving The EP0 and LTR Genes
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis P. Ribando
; STREET: 1815 No. 5352596th University Street
; CITY: Peoria
; STATE: IL
; COUNTRY: USA
; ZIP: 61604
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/945,283
; FILING DATE: 19920911
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Ribando, Curtis P
; REGISTRATION NUMBER: 27976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 309-685-4011 ext. 513
; TELEFAX: 309-685-4128
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8438 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Pseudorabies virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 622..6495
; FEATURE:
; NAME/KEY: variation
; LOCATION: replace(1099, "g")
; FEATURE:
; NAME/KEY: variation
; LOCATION: replace(1267, "e")
; FEATURE:
; NAME/KEY: variation
; LOCATION: replace(1381, "c")
; FEATURE:
; NAME/KEY: variation
; LOCATION: replace(1566, "c")
; FEATURE:
; NAME/KEY: variation
; LOCATION: replace(7010, "g")
; US-07-945-283-1

Query Match 1.3%; Score 41.6; DB 1; Length 8438;
Best Local Similarity 48.1%; Pred. No. 0.54;
Matches 148; Conservative 0; Mismatches 159; Indels 1; Gaps 1;

QY 132 CCGGTCCAGGCTGCGGAGTCGAGGCGAGGAGCGCGCTGATGACAGATCC 191
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 4305 CCAGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCCGCGCTCCGCGCGCTCC 4246

QY 192 AGAGCGGTGCGCGCGCGAGACTGCGCGTCCGCCGTCGACACCGCGCGCGCATGCCAG 251
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 4245 AGCCCGCGACAGCAAGTCCGCTCCAGCACCAAGTCCGCGACCAAGTCCGCGC 4186

QY 252 TTGCGCGCGCGCTGCTGATGAGGCGCGCTCCATATGAGGCTCATGCGCTACCAA 311
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 4185 CTCGCGGCTCCTCGGCTAGCGACGCTCCCGCGCGCGCGCGAGCCGCGC-CCGA 4127
```

Qy 312 GGAGTGGCCAAAGGACATCGGGCGGTGTGTCTCCCGCCGTGGAATGGCCATCGA 371  
Db 4136 GCGGGCAAGAAAGACCCCGCGCCGCGGGCCCGCCCGCGCGAGGAGA 4067  
Qy 3712 GCAGATCCGACAGGACTCTGCTGCGCCCTACTTCTCGACCTGGGGCTCTATGACAC 431  
Db 4066 CGAGGGGCTCTCGGCTCGGCTCTCGGAGCGCCACGCGACGACGAGA 4007  
Qy 432 GGAGTGC 439  
Db 4006 GGACCGG 3999

## RESULT 8

US-08-398-008A-1/c  
; Sequence 1, Application US/08398008A  
; Patent No. 5655588

; GENERAL INFORMATION:  
; APPLICANT: Kornbluth, Jacki  
; TITLE OF INVENTION: DNA Encoding Natural Killer Lytic Associated  
; TITLE OF INVENTION: Protein  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Gilbreth & Adler, P.C.  
; STREET: 8011 Candle Lane  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage  
; COMPUTER: MACINTOSH Iicl  
; OPERATING SYSTEM: Macintosh  
; SOFTWARE: Microsoft Word 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/398,008A  
; FILING DATE: March 2, 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/126,501  
; FILING DATE: 24-SEP-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Adler, Dr. Benjamin Aaron  
; REGISTRATION NUMBER: 35,423  
; REFERENCE/DOCKET NUMBER: D5705CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (713) 777-2321  
; TELEFAX: (713) 777-6908  
; TELEAX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2823 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double-stranded  
; TOPOLOGY: unknown  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: no  
; ANTI-SENSE: no  
US-08-398-008A-1

Query Match 1.3%; Score 41.6; DB 1; Length 2823;  
Best Local Similarity 44.7%; Pred. No. 0.32;  
Matches 161; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

Qy 2778 CCAGCGTGGCTGTCCCTCCAGCTCCCATCTCCACAGGCTACTCCCATCCATCGG 2837  
Db 559 CCAGCGACAGCGGACACTCTCTCCCGCCCGGGGCGACCGCTCGCGGCTCTCT 500  
Qy 2838 AGCGGTGAGCGGACGCTGTGTGAGCCCTGGGTGAGCCCGACGCGGACCGCGCACAG 2897  
Db 499 CATGTCGACCCAGGCTCCGCCCCCGCGCGGCGCTCGGCTCGGCGGCGG 440

Qy 2898 ACATGTGCCACCTCTCTCCGATCATGTCTCGGGCTGTAAAGGTGGAGGCTGGGC 2957  
Db 439 GCTCGCGGGGCAAGCGGCTCGGGCGGGGCTCTGGGCGCGGCGGCGGCGGCG 380  
Qy 2958 CCGGGGCTTCCCGCGGACAGAACCACTAGGAGAGGGGCTCTGTGAGAACACTGT 3017  
Db 379 GCGGGCGGAGCGGGGCGGGGCTCGGCTCGGCTTGGCCCCGGGGGCGGCGGC 320  
Qy 3018 CGGCTGTGCTGGGAGAGAGCTGGGACCATGCTGGCTCTCAGAGCACTCGGATGCG 3077  
Db 319 GGGCGGAGGAGAGAGAGAGCTGTGCAAGTGAAGGCGCGGCGCGCGCGCTGCGGC 260  
Qy 3078 ACTCAGGTGAGAGAGAGGCGGAGAGCTTGGCACCTGACCTCGAGCTTATTGT 3137  
Db 259 ACTTAGGCTGGGTCGGGCGCGCATGTAGCATGTGAGCGCGGCACTCGAGTCTTCT 200

## RESULT 9

US-08-893-333-1/c  
; Sequence 1, Application US/08893333A  
; Patent No. 5981705

; GENERAL INFORMATION:  
; APPLICANT: Kornbluth, Jacki  
; TITLE OF INVENTION: DNA Encoding Natural Killer Lytic Associated Protein  
; FILE REFERENCE: D5705CIP/D  
; CURRENT APPLICATION NUMBER: US/08/893,333A  
; CURRENT FILING DATE: 1997-07-16  
; NUMBER OF SEQ ID NOS: 17  
; SEQ ID NO 1  
; LENGTH: 2823  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; LOCATION: 190..1953  
; OTHER INFORMATION: CDS  
US-08-893-333-1

Query Match 1.3%; Score 41.6; DB 4; Length 2823;  
Best Local Similarity 44.7%; Pred. No. 0.32;  
Matches 161; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

Qy 2778 CCAGCGTGGCTGTCCCTCCAGCTCCCATCTCCACAGGCTACTCCATCCATCGG 2837  
Db 559 CCAGGACAGAGGACACTCTCTCCCGCGGGCGGCGGCGGCGGCGGCTCTCT 500  
Qy 2838 AGCGGTGAGCGGACGCTGTGTGAGCCCTTGGGTGAGCCCGACGCGGCGGCGAG 2897  
Db 499 CATGTCGACCCAGGCTCCGCCCCCGCGCGGCTCTCGGCTCGGCGGCGG 440  
Qy 2898 ACATGTGCCACCTCTCTCCGATCATGTCTCGGGCTGTAAAGGTGGAGGCGCTGGGC 2957  
Db 439 GCTCGGGGCGGAGCGGCTCGGGGCGGGGCTCTGGGCGCGGCGGCGGCGGCG 380  
Qy 2958 CCGGGGCTTCCCGCGGACAGAACCACTAGGAGAGGGGCTCTGTGAGAACACTGT 3017  
Db 379 GCGGGCGGAGCGGGGCGGGGCTCGGCTCGGCTTGGCCCCGGGGGCGGCGGC 320  
Qy 3018 CGGCTGTGCTGGGAGAGAGCTGGGACCATGCTGGCTCTCAGAGCACTCGGATGCG 3077  
Db 319 GGGCGGAGGAGAGAGAGCTGTGCAAGTGAAGGCGGCGGCGCGCGCTGCGGC 260  
Qy 3078 ACACAGGTGAGAGAGGCGGAGGAGAGCTTGGCACCTGACCTCGAGCTTATTGT 3137  
Db 259 ACTTAGGCTGGGTCGGGCGCGCATGTAGCATGTGAGCGCGGCACTCGAGTCTTCT 200

RESULT 10  
US-07-884-811-15/c  
; Sequence 15, Application US/07884811  
; Patent No. 5316921  
; APPLICANT: Godowski, Paul J. Lokker, Nathalie A. Mark, Melanie R.

```

; TITLE OF INVENTION: SINGLE-CHAIN HEPATOCYTE GROWTH FACTOR VARIANTS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/884,811
; FILING DATE: 19920518
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: 735.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10596 bases
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-884-811-15

Query Match 1.3%; Score 40.6; DB 1; Length 10596;
Best Local Similarity 50.2%; Pred. No. 1.1;
Matches 126; Conservative 0; Mismatches 124; Indels 1; Gaps 1;

QY 189 TCACAGAGCGGTGCGCCCAAGAACATGCGCGGTGCGCCCGTGACACCCCGCGCGCCATGCC 248
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2464 TCCTGCCCCCTCTGCTGCCCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2405
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 249 CAGTGGCCCGGCGGCTGTGCTAGCGGCCG-GCTCTCATGATGGGCTCATGCGGCTCA 307
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2404 CCCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTCC 2345
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 308 CCAGAGAGGTGGCCAAAGGACAGATCGGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTCA 367
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2344 TCCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2285
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 368 TCGAGCAGATCGGCAAGCAGTCACTCTGCGCCCTACTTCTGAGACTGGGCTATG 427
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2284 TCCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2225
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 428 ACACGAGGTGC 438
    ||| ||| |||
DB 2224 ACCGTGGGTCC 2214
    ||| ||| |||

RESULT 11
US-07-885-971-15/c
; Sequence 15, Application US/07885971
; Patent No. 5328837
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J., Lokker, Nathalie A., Mark, Melanie R.
; TITLE OF INVENTION: HEPATOCYTE GROWTH FACTOR PROTEASE DOMAIN VARIANTS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
```

```

; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/885,971
; FILING DATE: 19920518
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: 779
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10596 bases
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-885-971-15

Query Match 1.3%; Score 40.6; DB 1; Length 10596;
Best Local Similarity 50.2%; Pred. No. 1.1;
Matches 126; Conservative 0; Mismatches 124; Indels 1; Gaps 1;

QY 189 TCACAGAGCGGTGCGCCCAAGAACATGCGCGGTGCGCCCGTGACACCCCGCGCGCCATGCC 248
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2464 TCCTGCCCCCTCTGCTGCCCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2405
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 249 CAGTGGCCCGGCGGCTGTGCTAGCGGCCG-GCTCTCATGATGGGCTCATGCGGCTCA 307
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2404 CCCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTCC 2345
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 308 CCAGAGAGGTGGCCAAAGGACAGATCGGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTCA 367
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2344 TCCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2285
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 368 TCGAGCAGATCGGCAAGCAGTCACTCTGCGCCCTACTTCTGAGACTGGGCTATG 427
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2284 TCCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2225
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 428 ACACGAGGTGC 438
    ||| ||| |||
DB 2224 ACCGTGGGTCC 2214
    ||| ||| |||

RESULT 12
US-08-087-783A-15/c
; Sequence 15, Application US/08087783A
; Patent No. 5547856
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J., Lokker, Nathalie A., Mark, Melanie R.
; TITLE OF INVENTION: HEPATOCYTE GROWTH FACTOR VARIANTS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
```





```
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,087
FILING DATE: 18-May-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 779
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
TELEX: 910/371-7168
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ. ID NO: 15:
LENGTH: 10596 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-194-087-15
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Query Match          1.3%; Score 40.6; DB 3; Length 10596;
Best Local Similarity 50.2%; Pred. No. 1.1;
Matches 126; Conservative 0; Mismatches 124; Indels 1; Gaps 1;
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```
QY 189 TCCAGAGCCGTGCGCCCGCCAGAACTGCGGCTCCGCCCGCCGACCCCGCGGCCCATGCC 248
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2464 TCCGTGCCCCCTCCTGCTCCTGCTCCTGCTCCTGCTCCTGCTCCTGCTCCTGCTCCTG 2405

QY 249 CAGTTGCCCGCGCGGCTGCTGCTAGCGGCGC-6GCTCCATCATGGGCGCTCATGCGCTCA 307
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2404 CCTCTCTCTGCTCTCTGCTCCCTCTGCTCCCTCTGCTCCCTCTGCTCTGCTCTGCTCC 2345

QY 308 CCAAGAGGTGGCCAGAGGACATCGGCGCGGTGCTCCCGCGCGTGAAGTGAACGACCA 367
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2344 TCCGTGCTCCTGCGCCCTGCTGCGCCCTGCTGCGCCCTGCTGCGCCCTGCTGCTGCGCC 2285

QY 368 TCGAGCAGATCCGACAGAGTACTCTGCGCGCCCTACTCTCTGAGACTGCGGCTCATG 427
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DB 2284 TCCCTGCTCCTGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2225

QY 428 ACACGAGGTGC 438
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2224 ACCGTGGGTCC 2214
```

```
RESULT 15
US-09-130-114-1
: Sequence 1, Application US/09130114
: Patent No. 5976807
: GENERAL INFORMATION:
: APPLICANT: Horlick, Robert A.
: APPLICANT: Dama, Bassam B.
: APPLICANT: Robbins, Alan K.
: TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
: FILE REFERENCE: 0867/1D903051
: CURRENT APPLICATION NUMBER: US/09/130,114
: NUMBER OF SEQ. ID NOS: 36
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ. ID NO. 1
: LENGTH: 3452
: TYPE: DNA
: ORGANISM: VEBNA
US-09-130-114-1
```

```
Query Match          1.3%; Score 40.6; DB 4; Length 5452;
```

```
Best Local Similarity 50.2%; Pred. No. 0.79;
Matches 126; Conservative 0; Mismatches 124; Indels 1; Gaps 1;

QY 189 TCCAGAGCCGTGCGCCCGCCAGAACTGCGGCTCCGCCCGCCGACCCCGCGGCCCATGCC 248
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1921 TCCGTGCCCCCTCCTGCTCCTGCTCCTGCTCCTGCTCCTGCTCCTGCTCCTGCTCCTG 1980

QY 249 CAGTTGCCCGCGCGGCTGCTGCTAGCGGCGC-6GCTCCATCATGGGCGCTCATGCGCTCA 307
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1981 CCTCTCTCTGCTCTCTGCTCCCTCTGCTCCCTCTGCTCCCTCTGCTCTGCTCTGCTCC 2040

QY 308 CCAAGAGGTGGCCAGAGGACATCGGCGCGGTGCTCCCGCGCGTGAAGTGAACGACCA 367
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2041 TCCGTGCTCCTGCGCCCTGCTGCGCCCTGCTGCGCCCTGCTGCGCCCTGCTGCTGCGCC 2100

QY 368 TCGAGCAGATCCGACAGAGTACTCTGCGCGCCCTACTCTCTGAGACTGCGGCTCATG 427
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DB 2101 TCCCTGCTCCTGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2160

QY 428 ACACGAGGTGC 438
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2161 accgtggttc 2171
```

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Search completed: March 16, 2000, 11:12:08
Job time: 1088 sec
```

GenCore version 4.5  
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 16, 2000, 11:14:53 ; Search time 1755.56 Seconds  
(without alignments)  
6976.836 Million cell updates/sec

Title: US-09-211-755-1

Perfect score: 3244

Sequence: 1 TGACCTCGGGCAGGCTCTG.....CTTGCAAAAAAAAAAAAAA 3244

Scoring table: IDENTITY\_NUC

Searched: 4538634 seqs, 1887831982 residues

Database : EST:\*

Word size : 0

Number of hits that pass the threshold : 9077268

1: em\_est1:\*  
2: em\_est2:\*  
3: em\_est3:\*  
4: em\_est4:\*  
5: em\_est5:\*  
6: em\_est6:\*  
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18: em\_est18:\*  
19: em\_est19:\*  
20: gb\_est1:\*  
21: gb\_est2:\*  
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23: gb\_est4:\*  
24: gb\_est5:\*  
25: gb\_est6:\*  
26: gb\_est7:\*  
27: gb\_est8:\*  
28: gb\_est9:\*  
29: gb\_est10:\*  
30: gb\_est11:\*  
31: gb\_est12:\*  
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57: em\_est25:\*  
58: em\_est26:\*  
59: gb\_est33:\*  
60: gb\_est34:\*  
61: gb\_est35:\*  
62: gb\_est36:\*  
63: gb\_est37:\*  
64: gb\_est38:\*  
65: em\_est27:\*  
66: em\_est28:\*  
67: em\_est29:\*  
68: em\_est30:\*  
69: gb\_est39:\*  
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73: gb\_est43:\*  
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75: em\_est31:\*  
76: em\_est32:\*  
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78: em\_est34:\*  
79: gb\_gss1:\*  
80: gb\_gss2:\*  
81: gb\_gss3:\*  
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96: em\_gss9:\*  
97: em\_gss10:\*  
98: em\_gss11:\*  
99: gb\_gss10:\*  
100: gb\_gss11:\*  
101: em\_gss12:\*  
102: gb\_gss12:\*  
103: gb\_gss13:\*  
104: gb\_gss14:\*  
105: gb\_gss15:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	637.2	19.6	704	63	A1968032 wu12c11.x
C 2	557.4	17.2	560	45	A1341249 qx90d04.x
C 3	410.2	12.6	416	63	A1937563 wp78c11.x
C 4	408.2	12.6	414	47	A1500214 tm94a05.x
C 5	389.8	12.0	397	43	A1214087 ap29g06.x
C 6	368.2	11.4	384	40	A1000006 ot03b08.s
C 7	355.6	11.0	371	22	H14151 ym62d04.r1

C	8	320.4	9.9	346	20	2397.6	2397.6	HSC1HH042
C	9	315	9.7	321	20	2436.4	2436.4	HSC1HH041 n
C	10	258	8.0	368	20	T07621	T07621	EST05511 Fe
C	11	241.8	7.5	283	31	AA6128303	AA613872	no81126
C	12	235	7.2	235	36	AA613872	AA613872	no81126
C	13	223.6	6.9	853	87	AQ744524	AQ744524	H-5508_A
C	14	134	4.1	136	69	AM138313	AM138313	VI-H-Bit-1
C	15	132.2	4.1	302	27	AA022569	AA022569	ze70h11_r
C	16	121.4	3.7	544	42	AT134060	AT134060	GH11409_5
C	17	103	3.2	450	64	AL119755	AL119755	DKFZP761C
C	18	96.8	3.0	507	22	R76139	R76139	yi17b07_r1
C	19	94.8	2.9	512	64	AM049355	AM049355	VI-M-BH-1
C	20	92.2	2.8	404	35	AA567648	AA567648	HL01578_5
C	21	91	2.8	393	71	AM1568263	AM1568263	z39B08_x
C	22	83	2.5	459	61	AL042317	AL042317	DKFZP434N
C	23	82.6	2.5	900	87	AQ744512	AQ744512	HS_5508_A
C	24	82.2	2.5	619	46	AT404922	AT404922	GH24783_5
C	25	75	2.3	417	22	R80448	R80448	yi193c05_r1
C	26	71.2	2.2	599	46	AL403990	AL403990	GH2355_5
C	27	67	2.1	268	31	AA323988	AA323988	EST26929
C	28	66.2	2.0	611	26	X90542	X90542	HSG545 Hum
C	29	65.4	2.0	381	43	AT202961	AT202961	qr32c05_x
C	30	65.4	2.0	394	43	AT203251	AT203251	qr29c09_x
C	31	65.4	2.0	409	49	AI633778	AI633778	tt28d10_x
C	32	65.4	2.0	409	64	AM071653	AM071653	w94g05_x
C	33	65	2.0	925	79	CNS00919	AL050113	Drosoph111
C	34	64	2.0	895	79	CNS00717A	AL066286	Drosoph111
C	35	61.2	1.9	540	41	AL0663197	AL0663197	GH02730_5
C	36	61	1.9	492	26	X90543	X90543	HSG546 Hum
C	37	58	1.8	1101	79	CNS0019E	AL071370	Drosoph111
C	38	57.6	1.8	925	79	CNS0091P	AL050113	Drosoph111
C	39	56.4	1.7	398	27	AA036134	AA036134	mi175a09_r1
C	40	54.6	1.7	844	79	CNS0052P	AL056562	Drosoph111
C	41	52.6	1.6	932	79	CNS007420	AL066469	Drosoph111
C	42	52	1.6	479	42	AT108469	AT108469	GH07312_5
C	43	52	1.6	935	79	CNS006X	AL066051	Drosoph111
C	44	52	1.6	909	79	CNS001U	AL076720	Drosoph111
C	45	51.6	1.6	1009	79	CNS010EW	AL098882	Drosoph111

## ALIGNMENTS

RESULT	1
AI968032/c	
LOCUS	AI968032 704 bp mRNA EST 25-AUG-1999
DEFINITION	will2c11.x1 NCI-CGAP_GC6 Homo sapiens CDNA clone IMAGE:2516756 3 similar to TR:O75975 O75975 GABA-B RECEPTOR SPLICED VARIANT 2 ; , mRNA sequence.
ACCESSION	AI968032
VERSION	AI968032.1 GI:5764850
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 704)
TITLE	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> . National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
JOURNAL	Tumor Gene Index
COMMENT	Unpublished (1997)
CONTRACT	On Jun 5, 1998 this sequence version replaced gi:3189191.

Email: Robert.Strausberg@nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

```

www.bio.lnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 461.
Location/Qualifiers
1..704
FEATURES
SOURCE
```

/note="Vector: pT73D-Pac (Pharmacia) with a modified  
 polylinker; Plasmid DNA from the normalized library  
 NC1.GAP.GC4 was prepared, and ss circles were made in  
 vitro. Following HAP purification, this DNA was used as  
 tracer in a subtractive hybridization reaction. The driver  
 was PCR-amplified cDNAs from a pool of 5,000 clones made  
 from the same library (clonoids 1257096-1258631,  
 1469064-1470983, and 1475592-1476743). Subtraction by  
 Bento Soares and M. Fatima Bonaldo. "

Query Match	19.68;	Score 637.2;	DB 63;	Length 704;
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Best Local Similarity: 96.5%; Pred. No. 3e-139;  
Matches 682; Conservative 0; Mismatches 21; Indels 4; Gaps 3

2524 GAGCTGGATAAGACTTGGAGAGGTCACCATGCAAGCTGCAGGACACACCAGAAAGACC 2583

704 GAGCTGNATAAAGACTGGAAAGAGGTCACCCATGCAGCTGCAGTACACACAGNAAGA--C 647

Z384 ACCIACAI AAACAGAACAC IACCAAGAGC ICAAI GACAI CC ICAAC CIGGAGAAC IIC 204

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A vertical ruler with markings from 0 to 10 cm. The markings are in millimeters, with numbers every centimeter. The ruler is oriented vertically, with the 0 mark at the top and the 10 cm mark at the bottom.

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537 CTACCTGCAACACCTCTCCAAATCCAAAGTCTATTAGGACATATAAC 468

2764 TCTTCCAGAACACATCCAGCGTCGCGTCCTCCAGCTCCCATCCTCCACCAACGCCCTAC 2823

467 TCTCCAGAACATCCAGCGTCGGCTGTCCCTCCAGCTCCCATCCTCCACCAAGCCTAC 408

2824 CTCCATCATCGAGGCGTGGACGCCAGCTGTGTCAGCCCCCTGCGTCAGCCCCCACC GCC 2883

407 CTCCCATCCATCGGAGGCGTGGACGCCAGCTGTGTACAGCCCTGCGTACGCCCCACCGCC 348

2884 AGCCCCGCCACAGACATGTGCCACCCTCCTTCCGAGTCATGGTCTCGGGCCTGTAAAGG 2943

34 / AGCCCCGACACAGACAIGGCCACCCCTCTTCGAGTCAIGGCTCGGGCTGTTAGGG 208

[illegible]

\_\_\_\_\_

[illegible]

167 GAGGACATCCAGCTGACAGGAGCGAGACTTGGCACCAGC 108

3123 TCGAGCCTTATTGTGAAGTCCTTATTCTTCACAAGAAGAGGGAACCGGAATGGACGT 3182

107 TCGAGCCTTATTGTGAAGTCCCTATTCTTCACCAAGAAGAGGAAACGGAATGGACGT 48

QY 3183 CTCCTTAACATCTGCAACAAGAGGCGCTGGATATCAAACTTGC 3229  
 Db 47 CTCCTTAACATCTGCAACAAGAGGCGCTGGATATCAAACTTGC 1

RESULT 2  
 AI341249/c 560 bp mRNA EST 15-FEB-1999  
 LOCUS qx90d04.x1 NCI\_CGAP-GC6 Homo sapiens cDNA clone IMAGE:2009767 3',  
 DEFINITION mRNA sequence.  
 AI341249  
 ACCESSION AI341249.1 GI:4078176  
 VERSION EST.  
 KEYWORDS human.  
 SOURCE Homo sapiens  
 ORGANISM human.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 560)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT On Jan 14, 1998 this sequence version replaced gi:1798073.  
 Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert\_Strausberg@nih.gov  
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
 R. Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 www-bio.llnl.gov/bdrp/image/image.html

Insert Length: 1613 Std Error: 0.00  
 Seq primer: -400P from Glibco  
 High quality sequence stop: 452.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2009767"  
 /clone\_lib="NCI\_CGAP-GC6"  
 /tissue\_type="pooled germ cell tumors"  
 /lab\_host="DH10B"  
 /note="Vector: p773D-Pac (Pharmacia) with a modified  
 polylinker. Plasmid DNA from the normalized library  
 NCI-CGAP-GC4 was prepared, and ss circles were made in  
 vitro. Following HAP purification, this DNA was used as  
 tracer in a subtractive hybridization reaction. The driver  
 was PCR-amplified cDNAs from a pool of 5,000 clones made  
 from the same library (clonoids 1257096-125861,  
 1459064-1470983, and 1475592-1476743). Subtraction by  
 Bento Soares and M. Fatima Bonaldo."  
 BASE COUNT 102 a 144 c 180 g 133 t 1 others  
 ORIGIN

Query Match 17.28; Score 557.4; DB 45; Length 560;  
 Best Local Similarity 99.68; Pred. No. 1.5e-120;  
 Matches 558; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2670 CATTTAAAAATCAGTCGATCGAATCCCGACCTACGTGAGAACACAGAGCCCTC 2729  
 Db 560 CATTTAAANAATCAGTCGATCGAATCCCGACCTACGTGAGAACACAGAGCCCTC 501

QY 2730 TCGAACATGCAAGATCCTATAGAGATATAACTCTCAGAACATCCAGCGTCGGCT 2789  
 Db 500 TCGAACATGCAAGATCCTATAGAGATATAACTCTCAGAACATCCAGCGTCGGCT 441

QY 2790 GTCCCTCAGCTCCCATCTCTCCACCAAGCGCTACCTCCATCCATCGAGAGCGGTGAGCGC 2849

Db 440 GTCCCTCAGCTCCCATCTCTCCACCAAGCGCTACCTCCATCCATCGAGAGCGGTGAGCGC 381

QY 2850 CAGCTGTGTCAGGCCCTGTGTCAGCCGCCACCGCCAGCCCGCCACAGACATGTGCCAC 2909  
 Db 380 CAGCTGTGTCAGGCCCTGTGTCAGCCGCCACCGCCCGCCACAGACATGTGCCAC 321

QY 2910 CTCCTTCCGATCATGTGTCTCGGGCTGTGAAGGTGGAGGGCTGGGCCCGGGCTGCC 2969  
 Db 320 CTCCTTCCGATCATGTGTCTCGGGCTGTGAAGGTGGAGGGCTGGGCCCGGGCTGCC 261

QY 2970 CCGTGACAGAACCCACACTGGGGCAGAGAGGGTCTGTGCAGAAACACTGTGCGCTGTG 3029  
 Db 260 CCGTGACAGAACCCACACTGGGGCAGAGAGGGTCTGTGCAGAAACACTGTGCGCTGTG 201

QY 3030 CGGAGAGCTGGGGCACCACATGCGCTGTGACGACACTCGGATGGACTGTGCGCTGTG 3089  
 Db 200 CGGAGAGCTGGGGCACCACATGCGCTGTGACGACACTCGGATGGACTGTGCGCTGTG 141

QY 3090 AGGACGGGCGAGGGGAGAGACTGTGACCTGACCTGAGCCTTATTTGTAAGTCTTATT 3149  
 Db 140 AGGACGGGCGAGGGGAGAGACTGTGACCTGACCTGAGCCTTATTTGTAAGTCTTATT 81

QY 3150 TCTTCAAAAAGAGAGAAAGGAAATGGAGACGTCTTCAATCTGCAACAGAGAG 3209  
 Db 80 TCTTCAAAAAGAGAGAAATGGAGACGTCTTCAATCTGCAACAGAGAG 21

QY 3210 CGCTGGATATCAAACTTGC 3229  
 Db 20 CGCTGGATATCAAACTTGC 1

RESULT 3  
 AI937563/c 416 bp mRNA EST 06-SEP-1999  
 LOCUS wp/8q11.x1 NCI\_CGAP\_Brn25 Homo sapiens cDNA clone IMAGE:2467940 3',  
 DEFINITION similar to TR:075975 075975 GABA-B RECEPTOR SPLICED VARIANT 2 ;,  
 mRNA sequence.  
 AI937563  
 ACCESSION AI937563.1 GI:5676433  
 VERSION EST.  
 KEYWORDS human.  
 SOURCE Homo sapiens  
 ORGANISM human.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 416)  
 AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute / National Institute of Neurological  
 Disorders and Stroke, Brain Tumor Genome Anatomy Project  
 (CGAP/RTGAP), Tumor Gene Index  
 JOURNAL Unpublished (1998)  
 COMMENT On Jun 5, 1998 this sequence version replaced gi:3187952.  
 Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert\_Strausberg@nih.gov  
 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
 Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 www-bio.llnl.gov/bdrp/image/image.html

Seq primer: -400P from Glibco.  
 Location/Qualifiers  
 1..416  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2467940"  
 /clone\_lib="NCI\_CGAP\_Brn25"  
 /tissue\_type="anaplastic oligodendroglioma"

/lab\_host="DH10b"  
/note="Organ: brain; Vector: PT73D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' TGTACCAATCTGAAGTGGAGGCGCGCATGAGTTTATTTTATTTT T 3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 72 a 127 c 130 g 86 t 1 others

Query Match 12.6%; Score 410.2; DB 63; Length 416; Best Local Similarity 99.0%; Pred. No. 4.7e-86; Mismatches 4; Indels 0; Gaps 0; Matches 412; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2814 CCAGCCTACCTCCATCCATCGAGGCGTGTGACGCCAGTGTGTACAGCCCTGCTGAC 2873  
DB 416 CCAGCCTACCTCCATCCATCGAGGCGTGTGACGCCAGTGTGTACAGCCCTGCTGAC 357  
QY 2874 CCCACGCCCGACCCCGCCACAGACATGTGCCACCTCTCCGAGTCATGCTCGGG 2933  
DB 356 CCCACGCCCGACCCCGCCACAGACATGTGCCACCTCTCCGAGTCATGCTCGGG 297  
QY 2934 CCTGTAGGGTGGAGGCGTGGGCGGCGCTCCCGGTGACAGAACACATGCGGCGAG 2993  
DB 296 CCTGTAGGGTGGAGGCGTGGGCGGCGCTCCCGGTGACAGAACACATGCGGCGAG 237  
QY 2994 AGGGGTCTGTGCAGAAACACATGTGCGCTGTGCGTGCAGAGACTGGGACATGCTG 3053  
DB 236 AGGGGTCTGTGCAGAAACACATGTGCGCTGTGCGTGCAGAGACTGGGACATGCTG 177  
QY 3054 GCCTCTCAGACACTCGGATGACACTAGTGTGACAGAGCGGGGAGAGACTGG 3113  
DB 176 GCCTCTCAGACACTCGGATGACACTAGTGTGACAGAGCGGGGAGAGACTGG 117  
QY 3114 CACCTGACCTGAGCCTTATTGTGAAGTCTTATTCTTACAAAGAGAGAAAGGAA 3173  
DB 116 CACCTGACCTGAGCCTTATTGTGAAGTCTTATTCTTACAAAGAGAGAAAGGAA 57  
QY 3174 ATGGAGCGTCTTCTTAAACATCTGCAGCAAGGAGGCGTGGATATCAAACTTGC 3229  
DB 56 ATGGAGCGTCTTCTTAAACATCTGCAGCAAGGAGGCGTGGATATCAAACTTGC 1

RESULT 4  
A1500214/c 414 bp mRNA EST 14-APR-1999  
LOCUS tm94a05.x1 NCI\_CGAP\_Brn25 Homo sapiens cDNA clone IMAGE:2165744 3',  
DEFINITION mRNA sequence.  
ACCESSION A1500214  
VERSION A1500214.1 GI:4392196  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 414)  
NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute / National Institute of Neurological  
Disorders and Stroke, Brain Tumor Genome Anatomy Project  
(CGAP/BTGAAP). Tumor Gene Index  
Unpublished (1998)  
On Mar 20, 1998 this sequence version replaced gi:2980163.  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/BLINL at:  
[www.bio.linnl.gov/bhrp/image/image.html](http://www.bio.linnl.gov/bhrp/image/image.html)

Insert Length: 506 Std Error: 0.00  
Seq primer: -40UP from Gldco.  
Location/Qualifiers  
1. 414  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2165744"  
/clone\_lib="NCI CGAP Brn25"  
/tissue\_type="neoplastic oligodendrogloma"  
/lab\_host="DH10b"  
/note="Organ: brain; Vector: PT73D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' TGTACCAATCTGAAGTGGAGGCGCGCATGAGTTTATTTTATTTT T 3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 74 a 127 c 128 g 84 t 1 others

Query Match 12.6%; Score 408.2; DB 47; Length 414; Best Local Similarity 99.0%; Pred. No. 1.4e-85; Mismatches 4; Indels 0; Gaps 0; Matches 410; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2816 AGCCTACCTCCATCCATCGAGGCGTGTGACGCCAGTGTGTACAGCCCTGCTGAC 2875  
DB 414 AGCCTACCTCCATCCATCGAGGCGTGTGACGCCAGTGTGTACAGCCCTGCTGAC 355  
QY 2876 CCACGCCCGACCCCGCCACAGACATGTGCCACCTCTCCGAGTCATGCTCGGGCC 2935  
DB 354 CCACGCCCGACCCCGCCACAGACATGTGCCACCTCTCCGAGTCATGCTCGGGCC 295  
QY 2936 TGTAGGGTGGAGGCGTGGGCGGCGCTCCCGGTGACAGAACACATGCGGCGAG 2995  
DB 294 TGTAGGGTGGAGGCGTGGGCGGCGCTCCCGGTGACAGAACACATGCGGCGAG 235  
QY 2996 GGGTCTGTGCAGAAACACATGTGCGCTGTGCGTGCAGAGACTGGGACATGCTGC 3055  
DB 234 GGGTCTGTGCAGAAACACATGTGCGCTGTGCGTGCAGAGACTGGGACATGCTGC 175  
QY 3056 CTCTCAGACACTCGGATGACACTAGTGTGACAGAGCGGGGAGAGACTGGCA 3115  
DB 174 CTCTCAGACACTCGGATGACACTAGTGTGACAGAGCGGGGAGAGACTGGCA 115  
QY 3116 CCTGACCTGAGCCTTATTGTGAAGTCTTATTCTTACAAAGAGAGAGAGAAAT 3175  
DB 114 CCTGACCTGAGCCTTATTGTGAAGTCTTATTCTTACAAAGAGAGAGAGAAAT 55  
QY 3176 GGGAGCTCTTCTTAAACATCTGCAGCAAGGAGGCGTGGATATCAAACTTGC 3229  
DB 54 GGGAGCTCTTCTTAAACATCTGCAGCAAGGAGGCGTGGATATCAAACTTGC 1

RESULT 5  
A1214087 397 bp mRNA EST 21-OCT-1998  
LOCUS ap29g06.x1 Schiller astrocytoma Homo sapiens cDNA clone  
DEFINITION IMAGE:1956826 3' similar to TR:008621 008621 GABA-BRIB RECEPTOR. ;,  
mRNA sequence.  
ACCESSION A1214087  
VERSION A1214087.1 GI:3777688  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 397)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Gelsel, G., Jost, S., Kitzman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Merris, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.  
 WashU-NCI human EST Project  
 Unpublished (1997)  
 On Jan 17, 1998 this sequence version replaced gi:1900223.  
 CONTACT: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.wustl.edu  
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.  
 Possible reversed clone: similarity on wrong strand  
 Seq primer: -40UP from gldco  
 High quality sequence stop: 375.  
 Location/Qualifiers  
 1..397  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1956826"  
 /clone\_lib="Schiller astrocytoma"  
 /sex="male"  
 /tissue\_type="astrocytoma"  
 /dev\_stage="44 years"  
 /lab\_host="SOLR"  
 /note="Organ: brain; Vector: pBluescript SK- (Stratagene); site:1: EcoRI; site:2: XhoI; Double-stranded cDNA was prepared from human astrocytoma using primer 5'-GAGAGAGAGAGAGAGAGAGAGACTGCTGAGT(18)-3'. An EcoRI adaptor was used on the 5' end of the cDNA as follows: 5'-AATCGGCACGAG-3'. The library was size-selected and went through one round of amplification. Average insert size is 1.7 kb, with a range from 0.4-12 kb. Tumor identification by consensus pathology. This library was constructed by Dr. Martin Schiller (Johns Hopkins University)."  
 BASE COUNT 109 a 109 c 115 g 64 t  
 ORIGIN  
 Query Match 12.0%; Score 389.8; DB 43; Length 397;  
 Best Local Similarity 99.5%; Pred. No. 2.9e-81;  
 Matches 391; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Oy 1147 AAGCGGTGAGGGGGGGCCGCAAGTTCACAGGGGTACGCTCAGATGATCTGGGTC 1206  
 |||||||  
 Db 5 AAGCGGTGAGGGGGGGCCGCAAGTTCACAGGGGTACGCTCAGATGATCTGGGTC 64  
 Oy 1207 ATCGCAGACACTCAGAGGGCCATGGAGACACTGCATGCAGACGCGGCACACAGCG 1266  
 |||||||  
 Db 65 ATCGCAGACACTCAGAGGGCCATGGAGACACTGCATGCAGACGCGGCACACAGCG 124  
 Oy 1267 ATTCAGGACTTCACTACAGGACCAACGCTGGGCGAGATCCTCAATGCAATGCAAC 1336  
 |||||||  
 Db 125 ATCCAGGACTTCACTACAGGACCAACGCTGGGCGAGATCCTCAATGCAATGCAAC 184  
 Oy 1327 GAGACCACTTCTGGGGGTACCGGGTCAAGTGTATCCGAATGGGGAAGAAATGGG 1386  
 |||||||  
 Db 185 GAGACCACTTCTGGGGGTACCGGGTCAAGTGTATCCGAATGGGGAAGAAATGGG 244  
 Oy 1387 ACCATTAAATTACTCAATTTCAAGACAGAGGAGTGAAGGTGGAGAGTACAAAGCT 1446  
 |||||||  
 Db 245 ACCATTAAATTACTCAATTTCAAGACAGAGGAGTGAAGGTGGAGAGTACAAAGCT 304  
 Oy 1447 GTGGCCGACACACTGAGATCATCATGACACATCAGGTTCCAAAGATCCGAACACCA 1506  
 |||||||

Db 305 GTGGCCGACACACTGAGATCATCATGACACCAATCAGGTTCCAAAGATCCGAACACCA 364  
 Oy 1507 AAAGACAAGACATCATCTCTGGAGCAGCTGCGG 1539  
 |||||||  
 Db 365 AAAGACAAGACATCATCTCTGGAGCAGCTGCGG 397  
 RESULT 6  
 A1000006/c  
 LOCUS  
 DEFINITION  
 mRNA sequence.  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 384)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 Unpublished (1997)  
 On Jan 17, 1998 this sequence version replaced gi:1900928.  
 CONTACT: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert.Strausberg@nih.gov  
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
 www-bio.lnl.gov/dbfp/image/image.html  
 Seq primer: -40m13 fwd. ET from Amersham  
 High quality sequence stop: 321.  
 Location/Qualifiers  
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 /clone="IMAGE:1613751"  
 /clone\_lib="NCI-CGAP\_GC3"  
 /tissue\_type="pooled germ cell tumors"  
 /lab\_host="DH10B"  
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."  
 BASE COUNT 72 a 116 c 116 g 80 t  
 ORIGIN  
 Query Match 11.4%; Score 368.2; DB 40; Length 384;  
 Best Local Similarity 99.0%; Pred. No. 3.3e-76;  
 Matches 381; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
 Oy 2845 GAGGCCAGCTGTGTACAGCCCTCGCTCAGCCACCCAGCCAGCCCGCCACAGACATG 2904  
 |||||||  
 Db 384 GAGGCCAGCTGTGTACAGCCCTCGCTCAGCCACCCAGCCAGCCCGCCACAGACATG 325  
 Oy 2905 CCAACCTCTTCCGAGTCATGCTCGGCGCTGTAAAGGTGGAGGCTGCGCCGGGCG 2964  
 |||||||  
 Db 324 CCAACCTCTTCCGAGTCATGCTCGGCGCTGTAAAGGTGGAGGCTGCTGCTCC-GGCC 266  
 Oy 2965 CTCGCCGTGACAGAAACCACTGGGCGAGGGGCTGCTGTGAGAAACACTGCGGCTCT 3024  
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Db 265 CTCGCCCTGACAGAACCACTGGGAGAGGGTCTGCTGCAGAAACACTGTCGGCTCT 206

QY 3025 GGCTGGGAGAAAGCTGGGACCATGGCTGCTCAGAGACCATGGATGGACTCAGG 3084  
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Db 205 GGCTGGGAGAAAGCTGGGACCATGGCTGCTCAGAGACCATGGATGGACTCAGG 146  
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QY 3085 TGGACAGACGGGGGAGGGGAGACTTGGACCTGACCTGAGACCTTATTTGTGAAGTCC 3144  
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Db 145 TGGACAGACGGGGGAGGGGAGACTTGGACCTGACCTGAGACCTTATTTGTGAAGTCC 86  
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QY 3145 TTATTTCTTCAACAAAG 3204  
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Db 85 TTATTTCTTCAACAAAG 26  
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QY 3205 GGAGGCGCTGGATATCAACTGCG 3229  
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Db 25 GGAGGCGCTGGATATCAACTGCG 1

RESULT 7  
 H14151/c 371 bp mRNA EST 10-JUL-1995  
 LOCUS YME2d04.r1 Soares adult brain NZB4HB55Y Homo sapiens cDNA clone  
 DEFINITION IMAGE:163495 5', mRNA sequence.

ACCESSION H14151  
 VERSION H14151.1 GI:878971  
 KEYWORDS EST.

SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 1 (bases 1 to 371)  
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
 Trevisan, E., Waterston, R., Williamson, A., Wollmann, P. and  
 Wilson, R.

TITLE The WashU-Merck EST Project  
 JOURNAL Unpublished (1995)  
 COMMENT On Sep 21, 1992 this sequence version replaced gi:279426.  
 Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.edu  
 Insert Size: 1720  
 High quality sequence stops: 229  
 Source: IMAGE Consortium, LUNL  
 This clone is available royalty-free through LUNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Insert Length: 1720 Std Error: 0.00  
 Seq primer: M13RP1  
 High quality sequence stop: 229.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /db\_xref="GDB:583464"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:163495"  
 /clone\_lib="Soares adult brain NZB4HB55Y"  
 /sex="Male"  
 /dev\_stage="55-year old"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /note="Organ: brain; Vector: pTZ19 (Pharmacia) with a  
 modified polylinker. Site\_1: Not I; Site\_2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5'  
 TGTACCACTCTGAAGTGGAGCGCGCTTTTCTTTTCTTTT 3'],  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pTZ19 vector  
 (Pharmacia). Library went through one round of  
 normalization to a Cot = 53. Library constructed by Bento

Soares and M.Fatima Bonaldo. The adult brain RNA was  
 provided by Dr. Donald H. Gilden. Tissue was acquired  
 17-18 hours after death which occurred in consequence of a  
 ruptured aortic aneurysm. RNA was prepared from a pool of  
 tissues representing the following areas of the brain:  
 frontal, parietal, temporal and occipital cortex from the  
 left and right hemispheres, subcortical white matter,  
 basal ganglia, thalamus, cerebellum, midbrain, pons and  
 medulla."

BASE COUNT 60 a 99 c 106 g 99 t 7 others  
 ORIGIN

Query Match 11.0%; Score 355.6; DB 22; Length 371;  
 Best Local Similarity 97.0%; Pred. No. 3e-73; Indels 0; Gaps 0;  
 Matches 358; Conservative 0; Mismatches 11;

QY 968 AGGAGCCTTCTTGGTGGAGACAGTGCACACGGAGACCACTCATCCGCTCCTCGGA 1027  
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Db 369 AGCAGCCTTCTTGGTGGAGACAGTGCACACGGAGACCACTCATCCGCTCCTCGGA 310  
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QY 1028 AGAATCGCTTGGTGGCATTGAGAGGCTACATGGCTGATTTCCAGGCCCTGAGCTCCA 1087  
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Db 309 AGAATCGCTTGGTGGCATTGAGAGGCTAAATTGNCCTGATTTCCAGGCCCTGAGCTCCA 250  
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QY 1088 AGCAGATCAAGACCATCTCAGAAAGACTCCACAGCAGATGAGAGAGTACACACACA 1147  
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Db 249 AGCAGATCAAGACCATCTCAGAAAGACTCCACAGCAGATGAGAGAGTACACACACA 190  
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QY 1148 AGCGGTGAGCGGTGGGGCCCGCCAGCAAGTTCCAGGGTACGCTCAGATGGCATCGGTCA 1207  
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Db 189 AGCGGTGAGCGGTGGGGCCCGCCAGCAAGTTCCAGGGTACGCTCAGATGGCATCGGTCA 130  
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QY 1208 TCGCCCAAGACACTGACAGAGGGCCATGAGACACTGTGATCCGACGCGGACACGGGA 1267  
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Db 129 TCGCCCAAGACACTGACAGAGGGCCATGAGACACTGTGATCCGACGCGGACACGGGA 70  
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QY 1268 TCCAGGACTTCAACTACAGACACACACCGCTGGGAGATCATCTCATGGCATGGAAG 1327  
 |||||

Db 69 TCCAGGACTTCAACTACAGACACACACCGCTGGGAGATCATCTCATGGCATGGAAG 10  
 |||||

QY 1328 AGACCAACT 1336  
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Db 9 AGACCAACT 1

RESULT 8  
 Z39716/c 326 bp mRNA EST 07-NOV-1994  
 LOCUS HSCI1H04.2 normalized infant brain cDNA Homo sapiens cDNA clone  
 DEFINITION HSCI1H04.3', mRNA sequence.

ACCESSION Z39716  
 VERSION Z39716.1 GI:565511  
 KEYWORDS EST.

SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 1 (bases 1 to 326)  
 Aufray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C.,  
 Devignes, M.D., Duprat, S., Houligatte, R., Juneau, M.N., Lamy, B.,  
 Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pletu, G., Pouliot, Y.,  
 Sebastiani-Kabackchis, C. and Tessier, A.

TITLE IMAGE: molecular integration of the analysis of the human genome  
 and its expression  
 JOURNAL C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)  
 MEDLINE 95277534  
 COMMENT Contact: Genethon  
 Genethon  
 Genethon Centre de recherche sur le Genome Humain  
 1, rue de l'Internationale, Bp60 91002 EVRY Cedex, FRANCE  
 Tel: 33169472800  
 Fax: 33160778698



Email: genexpress@genethon.fr  
Single read: 27 T removed at sequence 5' end  
Genexpress\_library\_id: C; Genexpress\_sequence\_id: alc-1h04  
Seq primer: (-21)M13-universal.

FEATURES  
source

1. 326  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="C-1h04"  
/clone\_lib="normalized infant brain cdna"  
/sex="Female"  
/tissue\_type="total brain"  
/dev\_stage="3 months old"  
/note="Organ: brain; Vector: lafmid BA; Site\_1: HindIII;  
Site\_2: NotI; sex=Female; dev\_stage=3 months old;  
isolate=muscular atrophy patient; tissue\_type=total  
brain; total mRNA was oligo-(dT) primed and directionally  
cloned 5' -> 3' into the HindIII -> NotI sites of the  
lafmid BA vector. Clone library from B.Souares, Psychiatry  
Dept. Columbia University, USA. Normalization\_method:  
Bento Soares, P.N.A.S in press"

BASE COUNT 62 a 103 c 88 g 69 t 4 others  
ORIGIN

Query Match 9.9%; Score 320.4; DB 20; Length 326;  
Best Local Similarity 98.5%; Pred. No. 5.2e-65;  
Matches 321; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2904 GCACCCCTCCCTCCGATCATGTCTCGGGCCCTGAAGGTGGGAGCCCTGGGCCCGGGG 2963  
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Db 326 GCCACCTCTCTCCGANTCCTGCTCGGGCTGTANAGTGGGGGCGCTGGGCCCGGGG 267  
QY 2964 CCTCCCCCTGACAGAACACACTGGGAGGGGTCTGCTGAGAAACACTGTGGGCTC 3023  
|||||  
Db 266 CCTCCCCCTGACAGAACACACTGGGAGGGGTCTGCTGAGAAACACTGTGGGCTC 207  
QY 3024 TGGCTCGGGAAGCTGGGACCATGGCTGCTCTCAGACCACTGGATGGCACTCAG 3083  
|||||  
Db 206 TGGCTCGGGAAGCTGGGACCATGGCTGCTCTCAGACCACTGGATGGCACTCAG 147  
QY 3084 GTGGAGAGGAGGGGAGGGGAGACTTGGCACTCACTCGAGCTTTTGTGAAGTC 3143  
|||||  
Db 146 GTGGAGAGGAGGGGAGGGGAGACTTGGCACTCACTCGAGCTTTTGTGAAGTC 87  
QY 3144 CTATTCTTCAACAAGAGAGAGAAATGGAGCTTCTTCAATCATGTGCAACA 3203  
|||||  
Db 86 CTATTCTTCAACAAGAGAGAGAAATGGAGCTTCTTCAATCATGTGCAACA 27  
QY 3204 AGGAGCGCTGGGATATCAAACTTGC 3229  
|||||  
Db 26 AGGAGCGCTGGGATATCAAACTTGC 1

RESULT 9  
243654 243654 341 bp mRNA EST 14-NOV-1994  
LOCUS HSC1H041 normalized infant brain cdna Homo sapiens cdna clone  
DEFINITION c-1h04, mRNA sequence.  
ACCESSION 243654  
VERSION 243654.1 GI:572828  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 341)  
AUTHORS Auffray,C., Benar,G., Bois,F., Bouchier,C., da Silva,C.,  
Devignes,M.D., Duprat,S., Houligatte,R., Junneau,M.N., Lamy,B.,  
Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,  
Sebastien,Kabatchis,C. and Tessier,A.  
TITLE IMAGE: molecular integration of the analysis of the human genome  
and its expression

JOURNAL C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)  
MEDLINE 95277534  
COMMENT Contact: Genethon  
Genexpress-Genethon  
Genethon Centre de recherche sur le Genome Humain  
1, rue de l'Internationale, Bp60 91002 EVRY Cedex, FRANCE  
Tel: 33169472800  
Fax: 33160778698  
Email: genexpress@genethon.fr

FEATURES  
source

Single read  
Genexpress\_library\_id: C; Genexpress\_sequence\_id: ylc-1h04  
Seq primer: (-21)M13-universal.  
Location/Qualifiers  
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/tissue\_type="total brain"  
/dev\_stage="3 months old"  
/note="Organ: brain; Vector: lafmid BA; Site\_1: HindIII;  
Site\_2: NotI; sex=Female; dev\_stage=3 months old;  
isolate=muscular atrophy patient; tissue\_type=total  
brain; total mRNA was oligo-(dT) primed and directionally  
cloned 5' -> 3' into the HindIII -> NotI sites of the  
lafmid BA vector. Clone library from B.Souares, Psychiatry  
Dept. Columbia University, USA. Normalization\_method:  
Bento Soares, P.N.A.S in press"

BASE COUNT 87 a 102 c 83 g 66 t 3 others  
ORIGIN

Query Match 9.7%; Score 315; DB 20; Length 341;  
Best Local Similarity 98.8%; Pred. No. 9.8e-64;  
Matches 337; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 2191 GGGATGAGTGTCTACACAGTGGGATCATGTCATCGGGGCGCTGCTCCTTCCTG 2250  
|||||  
Db 1 GGGATGAGTGTCTACACAGTGGGATCATGTCATCGGGGCGCTGCTCCTTCCTG 60  
QY 2251 ACCGGGAGCAGCCCAATGTGCACTTGTGATCGTGGCTGTGTCATCATCTTGCAGC 2310  
|||||  
Db 61 ACCGGGAGCAGCCCAATGTGCACTTGTGATCGTGGCTGTGTCATCATCTTGCAGC 120  
QY 2311 ACCATCACCTCTGCTGCTGTATTTGTCGGAAGTCAATCACTTGAGACAAACAGAT 2370  
|||||  
Db 121 ACCATCACCTCTGCTGCTGTATTTGTCGGAAGTCAATCACTTGAGACAAACAGAT 180  
QY 2371 GCAGCAAGCAG-AACAGGGATTCAGTTCACAGCAATCAGAAAGAAAGATTCTTA 2429  
|||||  
Db 181 GCAGCAAGCAGAAACAGGGGATTCAGTTCACAGCAATCAGAAAGAAAGATTCTTA 240  
QY 2430 AAGCTCACCTGCTGCTCAGTGTGAACCAAGCAGCAATCCGGCT-GGAGGGCTTAC 2488  
|||||  
Db 241 AAGCTCACCTGCTGCTCAGTGTGAACCAAGCAGCAATCCGGCTGAGAGGGCTTAC 300  
QY 2489 AGTCAGAAAACCATCGCTGCAATGAAGTACACAGAGCTG 2529  
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Db 301 AGTCAGAAAACCATCGCTGCAATGAAGTACACAGAGCTG 341

RESULT 10  
T07621 368 bp mRNA EST 30-JUN-1993  
LOCUS EST05111 Fetal brain, Striatum (cat#936206) Homo sapiens cdna  
DEFINITION clone HFBEL81, mRNA sequence.  
ACCESSION T07621  
VERSION T07621.1 GI:318770  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

REFERENCE 1 (bases 1 to 368)  
 AUTHORS Adams M.D., Kerlavage, A.R., Fields, C. and Venter, J.C.  
 TITLE 3,400 expressed sequence tags identify diversity of transcripts  
 JOURNAL Nature Genet. 4, 256-267 (1993)  
 MEDLINE 93364420  
 COMMENT Contact: Adams, MD  
 The Institute for Genomic Research  
 932 Clopper Road, Gaithersburg, MD 20878  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: mdadams@tigr.org  
 Seq primer: M13-21.

FEATURES  
 source  
 1..368  
 /organism="Homo sapiens"  
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 /db\_xref="taxon:9606"  
 /clone="HBBEL81"  
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 /note="Vector: LambdaZAP-II: 17-18 wk gestation, female;  
 oligo-dT + random primed cDNA synthesis; lambdaZAP-II  
 vector, 1.0kb average inser size."  
 vector, 1.0kb average inser size." 3 others

BASE COUNT 91 a 94 c 79 g 101 t

ORIGIN

Query Match 8.0%; Score 258; DB 20; Length 368;  
 Best Local Similarity 94.8%; Pred. No. 2.5e-50;  
 Matches 289; Conservative 0; Mismatches 11; Indels 5; Gaps 2;

QY 1543 ATCCCTACCTCTCTACAGATCTCTGCGCTACCATCTCGGAGATGATGATGCGC 1602  
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 DB 1 ATCCCTACCTCTCTACAGATCTCTGCGCTACCATCTCGGAGATGATGATGCGC 60  
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QY 1603 AGTGCCTTTCTCTTCTTCAACATCAGAACCGGAGATGAGAGTCAATAAAGATGCGAGT 1662  
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 DB 61 AGTGCCTTTCTCTTCTTCAACATCAGAACCGGAGATGAGAGTCAATAAAGATGCGAGT 120  
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QY 1663 CCATACATGAACACCTATCATCTGAGGAGATGCTTCCATATGTTCCATATTTCTC 1722  
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 DB 121 CCATACATGAACACCTATCATCTGAGGAGATGCTTCCATATTTCTC 180  
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QY 1723 TTGGCCTTGATGATCCTTGTCTGAAAAAGACCTTTGAAACACTTTCACCGTCAGG 1782  
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 DB 181 TTGGCCTTGATGATCCTTGTCTGAAAAAGACCTTTGAAACACTTTCACCGTCAGG 240  
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QY 1783 ACCT-GGATTCCTACCGTGGGCT---ACAAGACCGCTTTTGGGGCCATGTTGCAAGA 1837  
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 DB 241 ACCTGGATTCCTACCGTGGGCTTACAGACCGCTTTTGGGGCCATGTTGCAAGA 300  
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QY 1838 CCTGG 1842  
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DB 301 CCTGG 305

RESULT 11  
 AA324303 283 bp mRNA EST 20-APR-1997  
 LOCUS EST27126 Cerebellum II Homo sapiens cDNA 5' end, mRNA sequence.  
 DEFINITION AA324303  
 ACCESSION AA324303  
 VERSION AA324303.1 GI:1976568  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 283)  
 AUTHORS Adams M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,  
 Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,  
 White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man, Wai, C.,  
 Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,

Fitzgerald, L.M., Fitzhugh, W.M., Fitchman, J.L., Geoghagen, N.S.,  
 Glodet, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,  
 Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaro, S.M., Merrick, J.M.,  
 Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,  
 Phillips, C.A., Ryder, S.E., Scott, J.L., Saudet, D.M., Shirley, R.,  
 Small, K.V., Spriggs, T.A., Utterback, T.R., Wetman, J.F., Li, Y.,  
 Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,  
 Dimke, D., Peng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,  
 He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,  
 Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weisner, P.S., Olsen, H.,  
 Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,  
 Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,  
 Fraser, C.M., and Venter, J.C.  
 Initial assessment of human gene diversity and expression patterns  
 based upon 83 million nucleotides of cDNA sequence  
 Nature 377 (6547 Suppl.), 3-174 (1995)

FEATURES  
 TITLE  
 JOURNAL Nature 377 (6547 Suppl.), 3-174 (1995)  
 MEDLINE 12140200  
 COMMENT On May 8, 1995 this sequence version replaced gi:801444.  
 Other ESTs: THC92772  
 Contact: Kerlavage, AR  
 Bioinformatics  
 The Institute for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850 USA  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: arkerlav@tigr.org  
 For clone availability, additional sequence and expression  
 information related to this EST, please check the TIGR Human Gene  
 Index (<http://www.tigr.org/tdb/hgi/hgi.html>)  
 Seq primer: M13 Reverse.

FEATURES  
 source  
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 /db\_xref="taxon:9606"  
 /clone\_lib="Cerebellum II"  
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 /dev\_stage="adult"  
 /note="Organ: brain; Vector: pBluescript SK-; Site\_1:  
 EcoRI; Site\_2: XhoI"

BASE COUNT 59 a 82 c 75 g 64 t 3 others

ORIGIN

Query Match 7.5%; Score 241.8; DB 31; Length 283;  
 Best Local Similarity 95.7%; Pred. No. 1.4e-46;  
 Matches 268; Conservative 0; Mismatches 10; Indels 2; Gaps 2;

QY 1990 GAGAGTACAGATGAGACCGGACCCAGACGAGATATCTCATCGCCCTCTCTCTG 2049  
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 DB 1 GAGAGTACAGATGAGACCGGACCCAGACGAGATATCTCATCGCCCTCTCTCTG 60  
 |||||||

QY 2050 GAGCAGCTGAGAACACCCATATGACCATGCGTGGCATCGTATGCTCAAGGA 2109  
 |||||||  
 DB 61 GAGCAGCTGAGAACACCCATATGACCATGCGTGGCATCGTATGCTCAAGGA 120  
 |||||||

QY 2110 CTTTCATGTTGTTGGGTTGTTCTTCTAGCTTGGAGACCGGCAAGTCAAGATCCCGCA 2169  
 |||||||  
 DB 121 CTTTCATGTTGTTGGGTTGTTCTTCTAGCTTGGAGACCGGCAAGTCAAGATCCCGCA 180  
 |||||||

QY 2170 CTCAAGCAGACGATACATGCGGATGAGTGTCTACAAGT-GGGATCATGTGCATCAT 2228  
 |||||||  
 DB 181 CTCAAGCAGACGATACATGCGGATGAGTGTCTACAAGTGGGGGATCATGTGCATCAT 240  
 |||||||

QY 2229 CGGGGGCGG-CGTCTCCTTCTGACCGGGGACGACGCCAA 2267  
 |||||||  
 DB 241 CGGGGGCGGCTTCTCTTCTCTGACCGGGGACGACGCCAA 280  
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RESULT 12  
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 LOCUS AA613872c  
 DEFINITION no81f06.s1 NCI\_CGAP\_AAI Homo sapiens cDNA clone IMAGE:1113251 3',

mRNA sequence.  
 AA613872  
 VERSION  
 AA613872.1 GI:2466006  
 EST.  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE  
 1 (bases 1 to 235)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 AUTHORS  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 TITLE  
 Unpublished (1997)  
 JOURNAL  
 On May 18, 1995 this sequence version replaced gi:811266.  
 COMMENT  
 Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert.Strausberg@nih.gov  
 Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: Stratagene, Inc., David B. Krizman,  
 Ph.D.  
 cDNA Library Arraying: Greg Lennon, Ph.D.  
 DNA sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

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 High quality sequence stop: 228.  
 Location/Qualifiers  
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 /tissue\_type="adrenal adenoma"  
 /lab\_host="SOLR (kanamycin resistant)"  
 /note="Organ: adrenal gland; Vector: Bluescript SK-;  
 Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally.  
 Primer: Oligo dT. Two pooled bulk adrenal adenomas. 5'  
 adaptor sequence: 5' GAATTCGACGAG 3' 3' adaptor  
 sequence: 5' CTCGAGTCTTTTCTTTT 3' Average insert  
 size: 1.6 kb."  
 45 a 73 c 58 g 59 t

BASE COUNT  
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 Query Match 7.2%; Score 235; DB 36; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 5e-45; Indels 0; Gaps 0;  
 Matches 235; Conservative 0; Mismatches 0;  
 Qy 2973 TGACAGAACACACTGGGAGAGGGTCTGCTCGAGAAACACTGTGGCTGTGGCTGGCG 3032  
 Db 235 TGACAGAACACACTGGGAGAGGGTCTGCTCGAGAAACACTGTGGCTGTGGCTGGCG 176  
 Qy 3033 AGAGCTGGGACCACTGGCTGGCTCTCAGGACCACTCGGATGGCACTCAGTGGACAGG 3092  
 Db 175 AGAGCTGGGACCACTGGCTGGCTCTCAGGACCACTCGGATGGCACTCAGTGGACAGG 116  
 Qy 3093 ACGGGGACGGGGAGACTTGGCACTTGACCTCGAGGCTTATTGTGAAGTCTCTTATTCT 3152  
 Db 115 ACGGGGACGGGGAGACTTGGCACTTGACCTCGAGGCTTATTGTGAAGTCTCTTATTCT 56  
 Qy 3153 TCACAAAGAGAGAACGGAATGGGACGTCTTCCTTAACATCTGCAACAAGGA 3207  
 Db 55 TCACAAAGAGAGAACGGAATGGGACGTCTTCCTTAACATCTGCAACAAGGA 1

RESULT 13  
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 LOCUS  
 DEFINITION HS\_5508\_A1\_D10\_177A RPCI-11 Human Male BAC Library Homo sapiens  
 853 bp DNA GSS 16-JUL-1999

genomic clone Plate-1084 Col-19 Row-G, genomic survey sequence.  
 AQ744524  
 VERSION  
 AQ744524.1 GI:5522046  
 GSS.  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE  
 1 (bases 1 to 853)  
 Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,  
 Kellier, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and  
 Hood, L.  
 Sequence-tagged connectors: A sequence approach to mapping and  
 scanning the human genome  
 Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)  
 99380589  
 CONTACT: Mahairas GG, Wallace JC, Hood L  
 High Throughput Sequencing Center  
 University of Washington  
 401 Queen Anne Avenue North, Seattle, WA 98109, USA  
 Tel: (206) 616-3618  
 Fax: (206) 616-3887  
 Email: jwallace@u.washington.edu  
 Clones are derived from the human BAC library RPCI-11. For BAC  
 library availability, please contact Pieter de Jong  
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from  
 BACPAC Resources ([http://bacpac.med.buffalo.edu/ordering\\_bac.htm](http://bacpac.med.buffalo.edu/ordering_bac.htm))  
 or from Research Genetics (<http://info@resgen.com>). BAC end Web Server:  
<http://www.htsc.washington.edu>  
 Plate: 1084 row: G column: 19  
 Seq primer: T7  
 Class: BAC ends  
 High quality sequence stop: 853.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="Plate-1084 Col-19 Row-G"  
 /clone\_lib="RPCI-11 Human Male BAC Library"  
 /sex="male"  
 /note="Vector: pBACe3.6; Genomic sequence of BAC ends"

BASE COUNT 224 a 211 c 200 g 215 t 3 others  
 ORIGIN  
 Query Match 6.9%; Score 223.6; DB 87; Length 853;  
 Best Local Similarity 94.2%; Pred. No. 4.5e-42;  
 Matches 243; Conservative 0; Mismatches 14; Indels 1; Gaps 1;  
 Qy 1095 CAAGACCATCTCAGGAAGACTCCACAGCAGTATGAGAGAGAGTACACACAAG-CGGT 1153  
 Db 465 CAATCCCTGTTTTCAGACCTCCACAGCAGTATGAGAGAGAGTACACACAAGCGCG 524  
 Qy 1154 CAGCGCTGGGGCCAGCAAGTTCCACGGGTACGCTACGATGGCATCTGGGTCTATCGCCA 1213  
 Db 525 CAGCGTGGGGCCAGCAAGTTCCACGGGTACGCTACGATGGCATCTGGGTCTATCGTCA 584  
 Qy 1214 AGACATGCAGAGGGCCATGGAGACACTGTCATGCCAGAGCGGACCGGATCCAGG 1273  
 Db 585 AGACATGCAGAGGGCCATGGAGACACTGTCATGCCAGAGCGGACCGGATCCAGG 644  
 Qy 1274 ACTTCAACTACAGGACCAACAGCTGGGCGAGGATCATCTCAATGCCATGAACAGACCA 1333  
 Db 645 ACTTCAACTACAGGACCAACAGCTGGGCGAGGATCATCTCAATGCCATGAACAGACCA 704  
 Qy 1334 ACTTCTTCGGGGTTCACGG 1351  
 Db 705 ACTTTTTCGGGGTTCACGG 722

RESULT 14  
 AW138313/c  
 LOCUS  
 AW138313 136 bp mRNA EST 29-OCT-1999

```

DEFINITION      UI-H-B11-acz-e-12-0-UI_s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone
IMAGE:2716127 3', mRNA sequence.
ACCESSION       AW138313
VERSION         AW138313.1  GI:6142631
KEYWORDS        EST.
SOURCE          human.
ORGANISM        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 136)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Jul 9, 1999 this sequence version replaced gi:5433571.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
The sequence contained an oligo-dr track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
NCI-CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/dbrrp/image/image.html
Seq primer: M13 Forward
POLYA=Yes.

FEATURES             Location/Qualifiers
     1..136
         /organism="Homo sapiens"
         /db_xref="taxon:9606"
         /clone="IMAGE:2716127"
         /lab_host="PH10B (Life Technologies)"
         /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The
NCI_CGAP_Sub3 library is a subtracted library derived from
the NCI_CGAP_Sub1 library, which is a subtracted library
derived from BI. BI constitutes a mixture of 21
normalized or subtracted NCI_CGAP libraries:
NCI_CGAP_Co4, NCI_CGAP_Pr22, NCI_CGAP_Pr28, NCI_CGAP_Co10,
NCI_CGAP_Co16, NCI_CGAP_Kid5, NCI_CGAP_Kid12,
NCI_CGAP_Kid3, NCI_CGAP_Kid11, NCI_CGAP_Lym2,
NCI_CGAP_Br2, NCI_CGAP_Co8, NCI_CGAP_CLL1, NCI_CGAP_Le12,
NCI_CGAP_Brn23, NCI_CGAP_Lu5, NCI_CGAP_Lu24,
NCI_CGAP_Lu19, NCI_CGAP_GC4, NCI_CGAP_GC6,
NCI_CGAP_Brn25. These 21 libraries were pooled and a
single-stranded DNA preparation of the resulting mixture
was used as a tracer in a subtractive hybridization with
a driver whose composition is detailed below:
NCI_CGAP_Kid3 pool 1    LHAM 3334-3337, 3682-3683,
3798-3803 (IMAGE CloneIDs 1322376-1323911,
1456008-1456775, 1500852-1502855); NCI_CGAP_Kid5 pool 1
LHAM 3338-3342, 3722-3725, 3776-3778 (IMAGE CloneIDs
1323912-1325831, 1471368-1472903, 1492104-1493255);
NCI_CGAP_Lu5 pool 1    LHAM 3575-3582, 3851-3854 (IMAGE
CloneIDs 1414920-1417991, 1520904-1522439); NCI_CGAP_GC4
pool 1    LHAM 3164-3167, 3716-3720, 3733-3735 (IMAGE
CloneIDs 1257096-1258631, 1469064-1470983,
1475592-1476743); NCI_CGAP_Pr22 pool 1    LHAM 2457-2459,
2758-2759, 3062-3068 (IMAGE CloneIDs 985608-986759,
1101192-1101959, 1217928-1220615); NCI_CGAP_Co10 pool 1
LHAM 2644-2653, 2871-2872 (IMAGE CloneIDs 1057416-1061255,
1144584-1145351). Subtraction was performed as previously
described [Bonaldo, Lennon & Soares (1996): Normalization
and Subtraction: Two Approaches To Facilitate Gene
Discovery. Genome Research 6, 791-806.
TAG_LIB=NCI_CGAP_Brn26
TAG_TISSUE=brain
TAG_SEQ=ATAGG"
     30 a      28 c      27 g      51 t
ORIGIN
```

```

Query Match      4.1%; Score 134; DB 69; Length 136;
Best Local Similarity 100.0%; Pred. No. 2e-21;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3111 TGGCACTGACCTCGAGCCCTATTCTGTAAGTCCTTATTTCTTCACAAAGAGGAAGCG 3170
|||||
Db 136 TGGCACTGACCTCGAGCCCTATTCTGTAAGTCCTTATTTCTTCACAAAGAGGAAGCG 77
|||||

QY 3171 GAAATGGAGCTCTTCTTAACATCTGCAAAACAAGGAGCGCTGGGATATCAAACTTGCA 3230
|||||
Db 76 GAAATGGAGCTCTTCTTAACATCTGCAAAACAAGGAGCGCTGGGATATCAAACTTGCA 17
|||||

QY 3231 AAAAAAAAAAAAAA 3244
|||||
Db 16 AAAAAAAAAAAAAA 3

RESULT 15
AA022569/c
LOCUS       AA022569          302 bp      mRNA          EST          30-JAN-1997
DEFINITION ze70h11.r1 Soares fetal heart_NDHH19W Homo sapiens cDNA clone
IMAGE:364389 5', mRNA sequence.
ACCESSION   AA022569
VERSION     AA022569.1  GI:1486659
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 302)
Hallier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
and Warra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wuston.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 984 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 136.
Location/Qualifiers
     1..302
         /organism="Homo sapiens"
         /db_xref="GDB:1281093"
         /db_xref="taxon:9606"
         /clone="IMAGE:364389"
         /clone_lib="Soares_fetal_heart_NDHH19W"
         /sex="unknown"
         /dev_stage="19 weeks"
         /lab_host="DH10B (ampicillin resistant)"
         /note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I oligo(dT) primer [5'
TGTACCAATCTGAAGTGGAGCGGCATCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot -5. Library constructed by
M.Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
```

```
BASE COUNT      60 a      92 c      97 g      46 t      7 others
ORIGIN

Query Match      4.1%; Score 132.2; DB 27; Length 302;
Best Local Similarity 82.2%; Pred. No. 7.8e-21;
Matches 175; Conservative 0; Mismatches 32; Indels 6; Gaps 2;

QY 56 GGGATTGCCCGACAT-CCTTCAGCGAAGTGCATGTGTGTTTGTAAACCA-----TCGTT 109
Db 302 GGGATTGCCCGACATCCCTTCAGCGAAGTGCATGTGTGTTTGTAAACCAATCGTTGGC 243
QY 110 GGCTGTCCGGAGACCGCGAGACCGGTCCAGGCTGCGGGAGTCGAGGCGGAGGAGAG 169
Db 242 TTGTCNGGGAGACCGCGAGGAGCGGTCCAGGCTGCGGGAGTCGAGGCGGAGGAGAG 183
QY 170 GCCCGTGTGAGTGCAGAGTCCAGAGCCGTGCGCCCCCAGAACTGCGGTCGCCCGCGTG 229
Db 182 GCCCGTGTGAGTGCAGAGTCCAGAGCCGTGCGCCCCCAGAACTGCGGTCGCCCGCGTG 123
QY 230 CACCCCGCGCGCATGCCCGAGTTGCCCGCGC 262
Db 122 ACCCCTGNGCGCATGCCCGAGTTGCCCGCGC 90
```

Search completed: March 16, 2000, 11:46:08  
Job time: 1875 sec



\*\*\*\*\*

## ALL

\*\*\*\*\*

Release 3.1A John F. Collins, Biocomputing Research Unit.

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protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Mar 15 21:27:39 2000: Maspar time 91.53 seconds

Tabular output not generated.

Title: >US-09-211-755-2

Description: (1-898) from US09211755.pep

Perfect Score: 6573

Scoring table: PAM 150

scoring centre.

Searched: 225878 seqs. 69334122 residues

Post-processing: Minimum Match 0%

Post processing. Minimum match of Listing first 45 summaries

Database: sptrembl12

Database:   
 1:sp\_archaea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human  
 5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle  
 9:sp\_phase 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified  
 13:sp\_vertebrate 14:sp\_virus  
 15:sp\_zoo

```
Statistics:
  Mean 54.327:  variance 102.961:  scale 0.528
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		ID	Description	Pred. No.
		Match	Length			
1	6499	98.9	941.4	075899	GABA-B RECEPTOR.	0.00e+00
2	6429	97.8	940.11	088971	GABA-B RECEPTOR GR2.	0.00e+00
3	2253	34.3	1221.5	09Y133	BCDNA.GH07312.	0.00e+00
4	1687	25.7	844.4	096022	GABAB RECEPTOR, SUBU1	0.00e+00
5	1687	25.7	839.4	095675	GABAB RECEPTOR, SUBU2	0.00e+00
6	1687	25.7	961.4	095375	GABA-B1A RECEPTOR.	0.00e+00
7	1682	25.6	832.11	092308	GABAB RECEPTOR 1D.	0.00e+00
8	1683	25.6	833.11	09W15	573K1.1.4 (GAMMA-AMINO	0.00e+00
9	1683	25.6	844.11	09W17	573K1.1.2 (GAMMA-AMINO	0.00e+00
10	1682	25.6	844.11	09W621	GABA-B1B1 RECEPTOR.	0.00e+00
11	1682	25.6	930.4	095468	GABABR1 PROTEIN.	0.00e+00
12	1683	25.6	960.11	09W18	573K1.1.1 (GAMMA-AMINO	0.00e+00
13	1682	25.6	960.11	09B620	GABA-B1A RECEPTOR.	0.00e+00
14	1681	25.6	960.11	09W048	GABA-B1A RECEPTOR.	0.00e+00
15	1352	20.6	662.11	09W16	573K1.1.3 (GAMMA-AMINO	3.12e-255
16	1351	20.6	875.11	09Z0F9	GABAB RECEPTOR 1C.	5.18e-255
17	1351	20.6	991.11	09Z004	GABAB RECEPTOR SUBTYPE	5.18e-255
18	1350	20.5	241.4	075975	GABA-B RECEPTOR SPLICE	8.61e-255
19	1167	17.8	182.4	075974	GABA-B RECEPTOR SPLICE	1.33e-214
20	722	11.0	402.5	023442	COSMID ZK180.	2.19e-118

Query Match 98.9%; Score 6499; DB 4; Length 941;  
Best Local Similarity 99.6%; Pred. No. 0.00e+00;

## ALIGNMENTS

RESULT	1	
ID	O75899	PRELIMINARY; PRT; 941 AA.
AC	O75899;	
DT	01-NOV-1998	(TReMBLrel. 08, Created)
DT	01-NOV-1998	(TReMBLrel. 08, Last sequence update)
DT	01-WAY-1999	(TReMBLrel. 10, Last annotation update)
DE	GABA-B RECEPTOR.	
DN	GABAB-R2.	
GN	Homo sapiens (Human).	
OS	Homo sapiens	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;	
CC	Eutheria; Primates; Catarrhini; Homnidae; Homo.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=BRAIN;	
RA	CLARK J.C., LAM A., BONNER T.I.;	
RT	"gb2, a second GABA-B receptor."	
RL	Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=CEREBELLUM;	
RA	WHITE J.H., WISE A., MAIN M.J., GREEN A., FRASER N.J., DISNEY G.H.,	
RA	BARNES A.A., EMSON P., FOORD S.M., MARSHALL F.H.;	
RT	"Heterodimerisation is required to form a functional GABAB receptor.";	
RL	Submitted (OCT-1998) to EMBL/GenBank/DBJ databases.	

Query Match 98.9%; Score 6499; DB 4; Length 941;  
Best Local Similarity 99.6%; Pred. No. 0.00e+00;

Matches		887; Conservative	3; Mismatches	1; Indels	0; Gaps	0;
Db	51	PSSPPLSLMGLMPLTKVAKSIGRGVLPAPVELAEIQIRNESLLRPFLDLRLYDTECDN	110			
Qy	8	SATGPLSLMGLMPLTKVAKSIGRGVLPAPVELAEIQIRNESLLRPFLDLRLYDTECDN	67			
Db	111	AKGLKAFYDAIKYGNHLMVGGVCPVTSIIAESLOGNVLQVLSFAATTPVLADKKYP	170			
Qy	68	AKGLKAFYDAIKYGNHLMVGGVCPVTSIIAESLOGNVLQVLSFAATTPVLADKKYP	127			
Db	171	YFRTVPSDNVNPAILKLLKHQWKRVGTLTQDVQRFSEVRNDLTGLVYGEDIEISDTE	230			
Qy	128	YFRTVPSDNVNPAILKLLKHQWKRVGTLTQDVQRFSEVRNDLTGLVYGEDIEISDTE	187			
Db	231	SFSNDPCTSVKLLKGNVRIILGQFDQNMAAKVFCCAYEENMYGSKYQWIIPGWYPSWW	290			
Qy	188	SFSNDPCTSVKLLKGNVRIILGQFDQNMAAKVFCCAYEENMYGSKYQWIIPGWYPSWW	247			
Db	291	EQVHTEANSSCLRNKLLAAMEGYIGVDPEPLSSKQIKTISGKTPQOYEREYNKRSGVG	350			
Qy	248	EQVHTEANSSCLRNKLLAAMEGYIGVDPEPLSSKQIKTISGKTPQOYEREYNKRSGVG	307			
Db	351	PSKHGAYDGIWIAKTLQAMETLHASSRHQRIQDFNYTDHTLGRILLNAMNETNFFG	410			
Qy	308	PSKHGAYDGIWIAKTLQAMETLHASSRHQRIQDFNYTDHTLGRILLNAMNETNFFG	367			
Db	411	VTGQVVFNGRMGTIKFTQDQREVKVGEYNVADTLEIINDTIRFQSEPPKDKTII	470			
Qy	368	VTGQVVFNGRMGTIKFTQDQREVKVGEYNVADTLEIINDTIRFQSEPPKDKTII	427			
Db	471	LEQRLKISLPLYSILSALTILGMIMASAFLEFNKRNQKLIKMSPPYMNLLIILGMLS	530			
Qy	428	LEQRLKISLPLYSILSALTILGMIMASAFLEFNKRNQKLIKMSPPYMNLLIILGMLS	487			
Db	531	YASIFLFLDGLDSFYSEKTFETLCTVTRTWILTGYTTAFGAMFAKTWRVHAIFKNVKKKK	590			
Qy	488	YASIFLFLDGLDSFYSEKTFETLCTVTRTWILTGYTTAFGAMFAKTWRVHAIFKNVKKKK	547			
Db	591	IKDQKLLVIVGGMLLDLCILICQAVDPLRRTVERYSMEPPDPAGRDISIRPLEHCEN	650			
Qy	548	IKDQKLLVIVGGMLLDLCILICQAVDPLRRTVERYSMEPPDPAGRDISIRPLEHCEN	607			
Db	651	THMTIWLGIYAYKGLLMFCFLAWETRNVSIPALNDSKYIGMSVYNGIMCIIGAAYS	710			
Qy	608	THMTIWLGIYAYKGLLMFCFLAWETRNVSIPALNDSKYIGMSVYNGIMCIIGAAYS	667			
Db	711	FLTRDQPNVQFCIVALVIFCSTITLCLVFVKLITLRTNPDAATQNRRFQTONOKKED	770			
Qy	668	FLTRDQPNVQFCIVALVIFCSTITLCLVFVKLITLRTNPDAATQNRRFQTONOKKED	727			
Db	771	SKTSTSVTQSVNQASTSRLEGLOSENHRLMKITELDKDLEEVMTQLODTEPKTYIKQNH	830			
Qy	728	SKTSTSVTQSVNQASTSRLEGLOSENHRLMKITELDKDLEEVMTQLODTEPKTYIKQNH	787			
Db	831	YOELNDILNLGNFTSTDDGKAILKNHLDONPOLQWNTPEPSRTCKDPIEDINSPEHIQ	890			
Qy	788	YOELNDILNLGNFTSTDDGKAILKNHLDONPOLQWNTPEPSRTCKDPIEDINSPEHIQ	847			
Db	891	RLSLQPLPILHHAYLPSIGGVADASCVPSCVPTASPRHRHVPSPSFRVMSGL	941			
Qy	848	RLSLQPLPILHHAYLPSIGGVADASCVPSCVPTASPRHRHVPSPSFRVMSGL	898			
RESULT 2						
ID	088871	PRELIMINARY;		PRT;	940 AA.	
AC	088871;					
DT	01-NOV-1998 (Tremblrel. 08, Created)					
DT	01-NOV-1998 (Tremblrel. 08, Last sequence update)					
DT	01-MAY-1999 (Tremblrel. 10, Last annotation update)					
DE	GABA-B RECEPTOR GBZ.					
OS	Rattus norvegicus (Rat).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;					
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.					

RN	SEQUENCE FROM N.A.						
RC	TISSUE=CEREBRAL CORTEX;						
RA	CLARK J.C., LAM A., BONNER T.I.;						
RT	*gb2, A second GABA-B receptor.;						
RL	Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.						
DR	EMBL; AF058795; AAC63994.1; -						
DR	PFAM; PF00003; 7tm3; 1.						
DR	PFAM; PF01094; ANF_receptor; 1.						
SQ	SEQUENCE 940 AA; 105762 MW; 94C83CC1 CRC32;						
	Query Match	97.8%;	Score 6429;	DB 11;	Length 940;		
	Best Local Similarity	97.8%;	Pred. No. 0.00e+00;				
	Matches	871;	Conservative	17;	Mismatches	3;	
				Indels	0;	Gaps	0;
Db	50	PSSPPLSLMGLMPLTKVAKSIGRGVLPAPVELAEIQIRNESLLRPFLDLRLYDTECDN	109				
Qy	8	SATGPLSLMGLMPLTKVAKSIGRGVLPAPVELAEIQIRNESLLRPFLDLRLYDTECDN	67				
Db	110	AKGLKAFYDAIKYGNHLMVGGVCPVTSIIAESLOGNVLQVLSFAATTPVLADKKYP	169				
Qy	68	AKGLKAFYDAIKYGNHLMVGGVCPVTSIIAESLOGNVLQVLSFAATTPVLADKKYP	127				
Db	170	YFRTVPSDNVNPAILKLLKHFRVRVGTLTQDXQRFSEVRNDLTGLVYGEDIEISDTE	229				
Qy	128	YFRTVPSDNVNPAILKLLKHQWKRVGTLTQDVQRFSEVRNDLTGLVYGEDIEISDTE	187				
Db	230	SFSNDPCTSVKLLKGNVRIILGQFDQNMAAKVFCCAFESMFGSKYQWIIIPGWYEPAMW	289				
Qy	188	SFSNDPCTSVKLLKGNVRIILGQFDQNMAAKVFCCAYEENMYGSKYQWIIIPGWYEPSWW	247				
Db	290	EQVHTEANSSCLRNKLLAAMEGYIGVDPEPLSSKQIKTISGKTPQOYEREYNKRSGVG	349				
Qy	248	EQVHTEANSSCLRNKLLAAMEGYIGVDPEPLSSKQIKTISGKTPQOYEREYNKRSGVG	307				
Db	350	PSKHGAYDGIWIAKTLQAMETLHASSRHQRIQDFNYTDHTLGRILLNAMNETNFFG	409				
Qy	308	PSKHGAYDGIWIAKTLQAMETLHASSRHQRIQDFNYTDHTLGRILLNAMNETNFFG	367				
Db	410	VTGQVVFNGRMGTIKFTQDQREVKVGEYNVADTLEIINDTIRFQSEPPKDKTII	469				
Qy	368	VTGQVVFNGRMGTIKFTQDQREVKVGEYNVADTLEIINDTIRFQSEPPKDKTII	427				
Db	470	LEQRLKISLPLYSILSALTILGMIMASAFLEFNKRNQKLIKMSPPYMNLLIILGMLS	529				
Qy	428	LEQRLKISLPLYSILSALTILGMIMASAFLEFNKRNQKLIKMSPPYMNLLIILGMLS	487				
Db	530	YASIFLFLDGLDSFYSEKTFETLCTVTRTWILTGYTTAFGAMFAKTWRVHAIFKNVKMKK	589				
Qy	488	YASIFLFLDGLDSFYSEKTFETLCTVTRTWILTGYTTAFGAMFAKTWRVHAIFKNVKMKK	547				
Db	590	IKDQKLLVIVGGMLLDLCILICQAVDPLRRTVERYSMEPPDPAGRDISIRPLEHCEN	649				
Qy	548	IKDQKLLVIVGGMLLDLCILICQAVDPLRRTVEKYSMEPPDPAGRDISIRPLEHCEN	607				
Db	650	THMTIWLGIYAYKGLLMFLGCFLAWETRNVSIPALNDSKYIGMSVYNGIMCIIGAAYS	709				
Qy	608	THMTIWLGIYAYKGLLMFLGCFLAWETRNVSIPALNDSKYIGMSVYNGIMCIIGAAYS	667				
Db	710	FLTRDQPNVQFCIVALVIFCSTITLCLVFVKLITLRTNPDAATQNRRFQTONOKKED	769				
Qy	668	FLTRDQPNVQFCIVALVIFCSTITLCLVFVKLITLRTNPDAATQNRRFQTONOKKED	727				
Db	770	SKTSTSVTQSVNQASTSRLEGLOSENHRLMKITELDKDLEEVMTQLODTEPKTYIKQNH	829				
Qy	728	SKTSTSVTQSVNQASTSRLEGLOSENHRLMKITELDKDLEEVMTQLODTEPKTYIKQNH	787				
Db	830	YOELNDILSLGNFTSTDDGKAILKNHLDONPOLQWNTTEPSRTCKDPIEDINSPEHIQ	889				
Qy	788	YOELNDILNLGNFTSTDDGKAILKNHLDONPOLQWNTTEPSRTCKDPIEDINSPEHIQ	847				
Db	890	RLSLQPLPILHHAYLPSIGGVADASCVPSCVPTASPRHRHVPSPSFRVMSGL	940				



QY 848 RLSLQPLHAYLPSIGVDASCPCVSPASPRHRHRVPPSFRVMVSGL 898

RESULT 3  
ID Q9Y133 PRELIMINARY; PRT: 1221 AA.  
AC O96022;  
DT 01-NOV-1999 (Tremblrel. 12, Created)  
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)  
DE BCDNA.GH07312.  
GN BCDNA.GH07312.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA RUBIN G.M., WAN K.H., HARVEY D., LEWIS S.E., BROKSTEIN P., TSANG G.,  
RA AKBAYANI A., ARCAINA T.T., BAXTER E., BLAZEJ R.G., BUTENHOFF C.,  
RA CHAMPE M., CHAVEZ C., CHEW M., DOYLE C.M., FARFAN D.E., FRISE E.,  
RA GALLE R., GEORGE R.A., HARRIS N.L., HOSKINS R.A., EVANS-HOLM J.M.,  
RA HOUSTON K.A., HUMMASTI S.R., KIM E., LI P., MOSHREFI M., PACLEB J.M.,  
RA PARK S., SEQUEIRA A., SETHI H., SNIR E., SVIRSKAS R.R., WEINBURG T.,  
RA CELNIKER S.E.;  
RT "Full length Drosophila melanogaster cDNA sequence."  
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF145639; AAD38614.1; -;  
SQ SEQUENCE 1221 AA; 138124 MW; CE3B7865 CRC32;

Query Match 34.3%; Score 2253; DB 5; Length 1221;  
Best Local Similarity 41.9%; Pred. No. 0.00e+00;  
Matches 325; Conservative 197; Mismatches 231; Indels 22; Gaps 18;

Db 21 AC-GRKASDVYIAGFPYDGVNSYTGRCVMSVSKALGHVNECHKILANRLHMMW 79  
QY 3 SCPARSAT-GPUSIMGLMPLTEKVAKGSTGRGVLPFAVEIAEQIRNES-LLRPFLDLURL 60  
Db 80 NDTQCNAAGVKSFFDMHSGKVMLEFGAACHTHYTDPIAKASKWHHTQLSYADTHPMF 139  
QY 61 YTECDNAGLKAFAFYDAIKYGNHLMVFGVCPSTSIASLQGNLVLSFAATPVL 120  
Db 140 T-KDAPNFRVVPSENAPRLALLKEFNWTRVGTVYQNEPRYSLPHNHVADLDAME 198  
QY 121 ADKKKYPYFRTVPSDNVNPAILKLLKHQWKRYGTLTQDVQVSEVRNDLTGLVLYGED 180  
Db 199 VEVETQSFVDSVSLKRLKREKVRILIGNFNEHFARKACEAYKLDWYGRAYOWLMA 258  
QY 181 IEISDTESEFSDPCTSVKRLKGNDRILGQDFDQNNAAKVFCCAYEENYKSKYQWIIIPG 240  
Db 259 TYSTDWNN-V-TQ-DSE-CSVSEIATALEGAILVDLLPLSTSGDITVAGITADEYLVEYD 314  
QY 241 WYEPSWQVHTSEANSRLRNLAAMEGYICVDFEPLSSKQIKTISGKTPOQYREYN 300  
Db 315 RLR-GTEYSRFGHYVDGWA-A-AL--AIQYV-AEKREDDLTTHDYRVKDWESVFLBAL 368  
QY 301 NRRSGVGSKFHYADYDGIWIAKTLQRAMETLHASSRQRIDQDFNYTDHTLGRILNAM 360  
Db 369 NRTSPGCVTPVRYNNERKANILINOLGOMEXIGEVSOKSHLDSLCKPVKWKCT 428  
QY 361 NETNFFGVTVQVFRNGERMGTKTFQDSDREVYKVEYNVAVADTLEI-INDTIRFQGE 419  
Db 429 PKDRTLIVIERHSONVNTIIVSASVIGVIAATVAFNFKYRNQYIKMSSPHLNNL 488  
QY 420 PKDKTILIEQLRKISLPLYSILSALTILGMIASAFNFKNKNQKILKMSPPMNL 479  
Db 489 IIVGCMYTLISIFGLDFTLSSVAFPYICTARAWILMAGSLSFSGAMFSKTRVHSIF 548  
QY 480 IILGGLSVASIFLGLDGSFVSEKTFETLCTVRTWILTVGTTAFGAMFAKTWRVHAIF 539  
Db 549 TDLKLNKKVICYQPLVMVGVLLADIALITWQADTPYRTKQLPLHLENID-DVLY 607  
QY 540 KNYMKKKIKDKOKLLVIGVGMILLDLICWQAVDPL-RRTEVKYSMEPDPAGRDISI 598

Db 608 IPENEYCSQSEHMTIFVSIYAYKGLLVFGAFWETRHVSIPALNDSKHIGFSYNNVFI 667  
QY 599 RPLLEHCENTHMTIWLGIYAYKGLLVFGCFLAWETRVNSIPALNDSKYIGMSYNNVGI 658  
Db 668 TCLAGAAISLVISDRKDLVFLVLSFIIFCTTATLCLVFPVKLVKRNQGVV-DKRV 726  
QY 659 MCIIIGAASFLTRDQPNVQFCIVALVIFCSITLCLVEVPKLTILRTNPDAAONRRFQ 718  
Db 727 ATLPRMSKNGRRDSSVCELEQ---RLRDKVNTNCRFKALMEKNELOALIRKL 777  
QY 719 FTQNKQKEDSTSTSVTSYNOASTSRLEGLQSENHRLMKITELDKDLBEVTMQL 773

RESULT 4  
ID O96022 PRELIMINARY; PRT: 844 AA.  
AC O96022;  
DT 01-MAY-1999 (Tremblrel. 10, Created)  
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)  
DE GABAB RECEPTOR, SUBUNIT 1B PRECURSOR.  
GN GABAB-R1 OR GABA-B R1B OR GABBR1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=CEREBELLUM;  
RA WHITE J.H., WISE A., MAIN M.J., GREEN A., FRASER N.J., DISNEY G.H.,  
RA BARNES A.A., EMSON P., FOORD S.M., MARSHALL F.H.;  
RT "Heterodimerisation is required to form a functional GABAB receptor."  
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=CEREBELLUM;  
RX MEDLINE; 99061981;  
RA KAUPMANN K., SCHULER V., MOSBACHER J., BISCHOFF S., BITTIGER H.,  
RA HEID J., FROESTL W., LEONHARD S., PFAFF T., KARSCHIN A., BETTLER B.;  
RT "Human gamma-aminobutyric acid type B receptors are differentially  
expressed and regulate inwardly rectifying K+ channels."  
RL Proc. Natl. Acad. Sci. U.S.A. 95:14991-14996(1998).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA YOUNGER R.;  
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ012186; CAA0940.1; -;  
DR EMBL: AJ225029; CAA12360.1; -;  
DR EMBL: AL031983; CAA21454.1; -;  
KW Signal; Receptor.  
FT SIGNAL 1 29 POTENTIAL.  
FT CHAIN 30 844 GABAB RECEPTOR, SUBUNIT 1B.  
SQ SEQUENCE 844 AA; 95148 MW; C7342B77 CRC32;

Query Match 25.7%; Score 1687; DB 4; Length 844;  
Best Local Similarity 36.2%; Pred. No. 0.00e+00;  
Matches 249; Conservative 180; Mismatches 243; Indels 16; Gaps 14;

Db 68 GOACQPAVEMALEDVNSRRDILPDYELKLHDSKDPQOATKYLYELLYNDPIKILMP 127  
QY 31 GRGVLPFAVEIAEQIRNE-SLLRPYFLDLRLDYDETCNAGLKAFAFYDAIKYGNHLMVFG 89  
Db 128 G-CSSVSTLVAEARMNVLIVSYGSSSPALSNRQRPFFTRTHPSATLHNPRVKLFEX 186  
QY 90 GVCPSVTIIAESLQGNLVLSFAATTPVLADKKYPYFRTVPSDNVNPAILKLLKH 149  
Db 187 WGKKIATIOQTEVFTSTLDDLEERVKEAGIEITRQSFSDPVPVKNLQDARIIV 246  
QY 150 YQWKRVGLTQDVQVSEVRNDLTGLVYGEDIEISDTESEFSDPCTSVKRLKGNDRVIL 209  
Db 247 GLFYETEARVCEVYKERLFGKYYVWFLIGVADNWF-KIY-DP-SINCTVDMEAVE 303  
QY 210 GQFDQNNAAKVFCCAYEENYKSKYQWIIIFGWEPFSEWQVHTSEANSRLRNLAAME 269  
Db 304 GHITTEIVMLNPANTRISNNTSQEFVEKLTIKRLKRHPETGGFGFAPLAYDAIWALALA 363



[illegible]

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RESULT 7
ID Q92308 PRELIMINARY; PRT; 812 AA.
AC Q92308;
DT 01-MAY-1999 (T-EMBLrel. 10, Created)
DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (T-EMBLrel. 10, Last annotation update)
DE GABAB RECEPTOR 1D.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
[1]
RN SEQUENCE FROM N.A.
RP RP
RC TISSUE=CEREBELLUM;
RX MEDLINE; 99092370.
RA ISOMOTO S., KAIBARA M., SAKURAI-YAMASHITA Y., NAGAYAMA Y., UEZONO Y.,
RA YANO K., TANIYAMA K.;
RT "Cloning and tissue distribution of novel splice variants of the rat
RT GABAB receptor";
RL Biochem. Biophys. Res. Commun. 253:10-15(1998).
DR EMBL; AB016161; BAA34709.1; -.
SQ RECEPTOR.
KW SEQUENCE. 812 AA; 90920 MW; 566BF90A CRC32;

Query Match 25.6%; Score 1682; DB 11; Length 812;
Best Local similarity 36.2%; Pred. No. 0.00e+00;
Matches 249; Conservative 178; Mismatches 245; Indels 16; Gaps 14;

Db 68 GQACOPAVEMALEDVNGRRDLPDYELKLHHDSKCDPGQATKYLYELYNDPKILMP 127
Qy 1: |||||:|::: | | |::: | | |::: | | |::: | | |:::
31 GRGVLPAVELAIEQIRNE-SLLRPYFLDLRYDTECNAGKGLAFYDAIKYGNHLMVFG 89

Db 128 G-CSSVSTLVAEARMWNLIVLSGSSSPALSNQRQPTFTFRHPSATLHNPVKLFKEK 186
Qy 1: |||||:|::: | | |::: | | |::: | | |::: | | |::: | | |:::
90 GVCPSFTIIAESLOGWNLVGSFAATPTVLADKKKYPYFRTVPSDNVNPAILKLKH 149

Db 187 GWKKKIAITQOTTEVFTSTLDLSERVKEAGIEITTFQSFSSPSOPAVPKMLKRQDARIIV 246

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Qy	150	YQWKRVGTLQDVQVORSEVRNDLTGVLGEDIETSEFSDNDPCTSYKKLGNDRVRIIL	209
Db	247	GLFYETEARVCFVEYKERLFGKKYVMFLIGWYADNWF-KTY-DP-SINCTVEEMTEAVE	303
Qy	210	GQPDQNAKVCCAEENMYGSKYQWIIIPGWYPSWQVTEANSSRCLRKNLLAAE	269
Db	304	GHIITEIVMLNPANTRSINWTSQEFVEKLTKLKRHPETGQFQAPLAYDAIWAALALA	363
Qy	270	GYIGVDFEPJSSKQIKTISOKTPOQY-ERYNN-KRSGVGPSKFH-G-YAYDIGIWIYAKT	325
Db	364	LNKTSGG-GRSGVRLEDFENYNNQITDQIYRAMNSSFEGVSGHVWFDASGRMAWLT	421
Qy	326	LORAMEIHLHSSRHORIODENYTDHTLGRILLNAMNETNFFGVTGQVVF-RNGERMGTIK	384
Db	422	IEQLOGGSYKKIGYDSTKODLSW-SKTDKWIIGSPPADOTLVIKTFRFLSQKLFTSVSY	480
Qy	385	FTQFQDSREVKVGYNVAVDLTLEIINDTIRFOGSEPPKDTIILEQLRKISLPLYSILSA	444
Db	481	LSSLGIVLAVCLFSFLNYNSHVRVYIONSQPNLANLTAVGCSLAAVAEPFLGDYGHIGRS	540
Qy	445	LTIIGMNASAFLEFNKRNKQIKLMSSPYMNNLILGMLSYASIFLFGLDGFSVSEK	504
Db	541	QPFVQCARLWLLGLGFSGLYGSMTKIKWVHTVFTKKEEKKSWRKTLPEWKLYATVGLL	600
Qy	505	TFETLCTVRTWLTWVYTTAFGAMFAKTRVHAIF-KNVKMK-KKIKDQKLLVIVGGM	561
Db	601	VGMVDVLILAIIQWIVDPJHRITIEFAKEEPEDIDVSTILPOLEHCSKKNNWTWLGIFYGK	660
Qy	562	LLIDLCILICQWAVDPLRRTVEKYSMEPPDPAGRDISIRPLEHCENTHTMIWIGUYVYK	621
Db	661	GLLLGLIFLAYETKYSVTEKINDHRAVGMAYINVAVLCLITAPVTMLSSQDDAAFAFA	720
Qy	622	GLMLFGCFLANETRWNSIPALNDSKVIKGSVYVNGIMCIIGAUVSELTQDQPNVQFCIV	681
Db	721	SLAIVFSSYITVLVLFVFKPMKRLITRGE	748
Qy	682	ALVIFICSTIILCVFVPKLTITRNP	709

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RESULT      8
ID          Q9WV15 PRELIMINARY; PRT; 833 AA.
AC          Q9WV15;
DT          01-NOV-1999 (TrEMBLrel. 12, Created)
DT          01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT          01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE          573K1.1.4 (GAMMA-AMINOBUTYRIC ACID (GABA) B RECEPTOR, 1D).
GN          573K1.1.
OS          Mus musculus (Mouse).
OC          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC          Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC          [1]
RC          SEQUENCE FROM N.A.
RA          YOUNGER R.;
RL          Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases..
DR          EMBL; AL078630; CAB44993.1; -.
KW          Receptor.
KW          SEQUENCE 833 AA; 93167 MW; 0C07A359 CRC32;

Query Match 25.6%; Score 1683; DB 11; Length 833;
Best Local Similarity 36.2%; Pred. No. 0.00e+00;
Matches 249; Conservative 178; Mismatches 245; Indels 16; Gaps

Db 68 GQACQAPVEMALEDVNSRRDILPDYELKLIHHSKCDPGQATKYLYELLNDPKIILMP 127
QY 31 GRGVLPVAVELATEIQIRNE-SLLRPYFLDLRLYDTECDNAKGLKAFYDAIKYGNPHLMVFG 89

Db 128 G-CSSVSTLVAEARMWNLVLVSYGSSPALSNQRQPTFFTRHPSATLHNPTRVKLFKEK 189
QY 90 GVCPSVTSIIAESLOGWNLVOLFSFAATTPVLADKKKYPFFRYTVPDSNAVNPAILKLLKH 149

Db 187 GWKKIATIQOETVFTTDLDDSERVKEAGIETTFROSFTSDPAVPYKNLKKRODAIIV 2148

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QY 150 YQWKRVGTLTQDQRFSEVRNDLTGVLGYGEDIESTSFSDNPDCTSVKKLKGNDRVRIIL 209
Db 247 GLFYETEARKEVCEVYKERLFGKKYVWFLIGYADNWF-KTY-DP-SINCTVEEMTEAVE 303
QY 210 GQFDQNMAAKVFCCAEEENYGSQKQWIIPGWYEPWSWEOVHTEANSSRCLRNKLLAAWE 269
Db 304 GHITTEIVMLNPANTRISNMTSQBEVEKLTKRLKRHPPEETGGQOEAPLAYDAIWAALALA 363
QY 270 GYIGVDFEPLSSKQIKTISGKTPOQY-EREYNN-KRSGVGPSKFH-G-YAYDGIWVIART 325
Db 364 LNKTSGG--GGRSGVRLEDFNNGTITDQIYRAMNSSSFEVSGHVYFDASGSRMAWTL 421
QY 326 LQAMETLHASSRHQIQDFNTDHTLGRILLANNEINFVGTQGVVF-RNGERMGTIK 384
Db 422 IEQLOGGSKKIGYDSTKDDLSW-SKTDKWIGGSPPADQTLVKTFRFLSKOKLISVSV 480
QY 385 FTQFQDSREVKVGEYNVADTLEIINDIRFQGSPPDKTIILQELKISLPLYSILSA 444
Db 481 LSSLGIVLAVCLSNFYNSHVRYIONOPNNLTAVGCSIALAAVPLGLDGYHIGRS 540
QY 445 LTILGIMASAFLEFNKRNOKLIKMSPYMNNLIILGMLSYASIFLFLDGSFVSEK 504
Db 541 QPPEVCOARLWLLGLGFSIGSGMETKIWWVHTVETKKEEKWKRTLEPWKLYATVGLL 600
QY 505 TPETLCTVTRTWLTGYTTAFGAMFAKTRVHAIF--KNVKMK-KKIIKDKQLLVIVGGM 561
Db 601 VGMDLTLTAIQVIDPLHRTIETFAKEPKEDIDVSIPLQLEHSCSKMNTWLGIIFYGK 660
QY 562 LUIDCILICIQAVDPLRRTVEKYSMEPDAGRDISIRPLEHCENTHMTIWLGIIVAYK 621
Db 661 GULLLGLIFLAYETKSVSTEKINDHRAVGMAYINAVLCLITAPVTMLSSQODAAFAFA 720
QY 622 GULMLFGCLAWETRNVISIPALNSKYIGMSVYNGIMCIIGAASVFLTRDQPNVQFCIV 681
Db 721 SLAIVFSSYITLVLFVFKMRRLITRGE 748
QY 682 ALVIFCSTITLCLVFPKLTILRTNPD 709

RESULT 9
ID Q9WV17 PRELIMINARY; PRT; 844 AA.
AC Q9WV17;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE 573K1.1.2 (GAMMA-AMINOBUTYRIC ACID (GABA) B RECEPTOR, 1B).
GN 573K1.1.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA YOUNGER R.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL078630; CAB44991.1; -.
KW Receptor.
SQ SEQUENCE 844 AA; 95022 MW; 96F2ED2A CRC32;

Query Match 25.6%; Score 1683; DB 11; Length 844;
Best Local Similarity 36.2%; Pred. No. 0.00e+00;
Matches 249; Conservative 178; Mismatches 245; Indels 16; Gaps 14;

Db 68 GOACOPAVEALEVDNSRRDILPDYELKLIHDSKCDPGQATKYVELLYNDPIKILMP 127
QY 31 GRGVLPAVELAIEQIRNE-SLLRPYFDLRLDYDETCENAKGLKAFDAIKYGNHILMVF 89
Db 128 G-CSSVSTLVAEARMNWLIVLSYSSSPALSNRQFPPTFRTHPSATLHNPTRVKLEK 186
QY 90 GVCPSVTSIIAIESLQGNLWVLSFAATTPVLADKKKYPYFRTVPSDNVNPAILKLLX 149
Db 187 WGWKKIATIQTTVEFTSTLDDLEERKEAGIEITRQSFSDPVPVNLKQKQDAIIV 246
QY 150 YQWKRVGTLTQDQRFSEVRNDLTGVLGYGEDIESTSFSDNPDCTSVKKLKGNDRVRIIL 209
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Db 247 GLFYETEARKEVCEVYKERLFGKKYVWFLIGYADNWF-KTY-DP-SINCTVEEMTEAVE 303
QY 210 GQFDQNMAAKVFCCAEEENYGSQKQWIIPGWYEPWSWEOVHTEANSSRCLRNKLLAAWE 269
Db 304 GHITTEIVMLNPANTRISNMTSQBEVEKLTKRLKRHPPEETGGQOEAPLAYDAIWAALALA 363
QY 270 GYIGVDFEPLSSKQIKTISGKTPOQY-EREYNN-KRSGVGPSKFH-G-YAYDGIWVIART 325
Db 364 LNKTSGG--GGRSGVRLEDFNNGTITDQIYRAMNSSSFEVSGHVYFDASGSRMAWTL 421
QY 326 LQAMETLHASSRHQIQDFNTDHTLGRILLANNEINFVGTQGVVF-RNGERMGTIK 384
Db 422 IEQLOGGSKKIGYDSTKDDLSW-SKTDKWIGGSPPADQTLVKTFRFLSKOKLISVSV 480
QY 385 FTQFQDSREVKVGEYNVADTLEIINDIRFQGSPPDKTIILQELKISLPLYSILSA 444
Db 481 LSSLGIVLAVCLSNFYNSHVRYIONOPNNLTAVGCSIALAAVPLGLDGYHIGRS 540
QY 445 LTILGIMASAFLEFNKRNOKLIKMSPYMNNLIILGMLSYASIFLFLDGSFVSEK 504
Db 541 QPPEVCOARLWLLGLGFSIGSGMETKIWWVHTVETKKEEKWKRTLEPWKLYATVGLL 600
QY 505 TPETLCTVTRTWLTGYTTAFGAMFAKTRVHAIF--KNVKMK-KKIIKDKQLLVIVGGM 561
Db 601 VGMDLTLTAIQVIDPLHRTIETFAKEPKEDIDVSIPLQLEHSCSKMNTWLGIIFYGK 660
QY 562 LUIDCILICIQAVDPLRRTVEKYSMEPDAGRDISIRPLEHCENTHMTIWLGIIVAYK 621
Db 661 GULLLGLIFLAYETKSVSTEKINDHRAVGMAYINAVLCLITAPVTMLSSQODAAFAFA 720
QY 622 GULMLFGCLAWETRNVISIPALNSKYIGMSVYNGIMCIIGAASVFLTRDQPNVQFCIV 681
Db 721 SLAIVFSSYITLVLFVFKMRRLITRGE 748
QY 682 ALVIFCSTITLCLVFPKLTILRTNPD 709

RESULT 10
ID O08621 PRELIMINARY; PRT; 844 AA.
AC O08621;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE GABA-BRIB RECEPTOR.
GN GABA-BRIB OR GABABR1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TIF (RAI F[SPF]); TISSUE-CORTEX, AND CEREBELLUM;
RX MEDLINE; 9722131.
RA KAUPMANN K., HEGGEL K., HEID J., FLOR P.J., BISCHOFF S., MICKEL S.J.,
RA MCMASTER G., ANGST C., BITTIGER H., FROESTL W., BETTLER B.;
RT "Expression cloning of GABA(B) receptors uncovers similarity to
RT metabotropic glutamate receptors.";
RL Nature 386:239-246(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-WISTAR;
RA PFAFF T., MALITSCHKE B., KAUPMANN K., BETTLER B., KARSCHIN K.;
RT "Alternative splicing generates a novel isoform of the rat
RT metabotropic GABA(B) receptor.";
RL Eur. J. Neurosci. 0:0-0(1999).
DR EMBL; Y10370; CAA71399.1; -.
DR EMBL; AF110797; AAD19657.1; -.
DR EMBL; AF110796; AAD19657.1; JOINED.
DR PFAM; PF00003; 7tm_3; 1.
DR PFAM; PF01094; ANF_receptor; 1.
KW Receptor.
SQ SEQUENCE 844 AA; 95037 MW; 6611F68D CRC32;
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Query Match		25.6%	Score 1682;	DB 11;	Length 844;
Best Local Similarity		36.2%	Pred. No. 0.00e+00;		
Matches 249;		Conservative 178;	Mismatches 240;	Indels 16; Gaps 14;	
Db	68	GOACOPAVEMALEDVNSRRDILPDYELKLIHDSKDCDQCATKYLYELLYNDPIKIILMP	127		
Qy	31	GRGVLPAVELAIEQIRNE-SLLRPYFDLRLYDTECDNAKGLKAFYDAIKYGNHLMVFG	89		
Db	128	G-CSSVSTLVAEARMNLIIVSYGSSSPALSNRQRFPTFFTHPSATLHNPTRVKLFKEK	186		
Qy	90	GVCPVTSIIAESLOGNVLQVLSFAATTPVLADKKKYPYFFRTVPSDNAVNPAILKLKH	149		
Db	187	WGKKIATIOOTTEVTSTLDLEERVKRKEAGIEITFRQSFSDPAPVKNLKRQDARIIV	246		
Qy	150	YQWKRVTGTLTDVQVRESEVNDLTGVLYGEDIEISDTESFSDNPTCSVKKLGNDRVIL	209		
Db	247	GLFYETEARVCEVYKERLFGKKYVWFLIGYADNWF-KTY-DP-SINCTVEEMTFAVE	303		
Qy	210	GQFDQNNAAKVFCCAYEENMYGSKYQWIIPGWYEPFQVTEANSRCLRNLLAAME	269		
Db	304	GHITTEIVMLNPANTRISNMTSQEFVEKLTKLKRHPETEGGFOEAPLAYDAIWAALA	363		
Qy	270	GYIGVDFEPLSSKOIKTISGKTPQY-EREYNN-KRSGVGPSKEH-G-YAYDGIWVIAT	325		
Db	364	LKNTSGG--GGRSGVRLDEFNYNQITDQIYRAMNSSSFEVSGVGHVYFDASGSRMAWTL	421		
Qy	326	LORAMETLHASSRHQRIOQDFNYDHTLGRILNANMETNFFGVGTQGVVF-RNGERMGTIK	384		
Db	422	IEQLOGGSYKIGYDSTKDDLSW-SKTDKWIIGSGPPADQTLVIKTFRLSKLFISVSV	480		
Qy	385	FTQFQDSREVKGVEYNADVTLEIINDTIRFQSEPPKDKTIILBOLRKISLPLYSILSA	444		
Db	481	LSSIGLIVAVCLSFNLYNSHVRVYIONSQPNLNLTAVGCSLALAAVPLGLDGYHIGRS	540		
Qy	445	LTILGMIMASAEFLFNKRNQKLMKSSPYNNLIILGMLSYASIFLFLDGSFVSEK	504		
Db	541	QFPFVCOARLWLLGLGFSLGYSNMFTKIWWHTVFTKKEEKWKRTLPKWLKYATVGLL	600		
Qy	505	TFETLCTVTRTWLTGVTYTAFAAMFAKTRVHAIF--KNVKMK-KKIIKDQKLLIVYVGM	561		
Db	601	VGMDVLTALWQIVDPLHRTIEFAKEEPEKEDIDVLSILPOLHSCSKKMTWLGIFGYK	660		
Qy	562	LLIDLCILICQAVDPLRRVYKESMEPPAGRODISIRPLEHCENTHMTWLGIVYAYK	621		
Db	661	GLLLGLGIFLAYETKSVSTEKINDHRAVGMAYINVAVLCLITAPVTMILSQDAAFAFA	720		
Qy	622	GLLMLFCFLAWETRNYSIPALNDSKYIGMSYVNVGIMCIIGAAVSFLTRDQPNVQFCIV	681		
Db	721	SLAIVFSSYITLVVLFVPMRRLITRGE	748		
Qy	682	ALVIFCSTLCLVFPKLTITLTPND	709		
RESULT 11					
ID	O95468	PRELIMINARY;	PRT;	930 AA.	
AC	O95468:				
DT	01-MAY-1999	(T-EMBLrel. 10, Created)			
DT	01-MAY-1999	(T-EMBLrel. 10, Last sequence update)			
DT	01-NOV-1999	(T-EMBLrel. 12, Last annotation update)			
DE	GABABRI PROTEIN.				
GN	GABABRI.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				
OC	Eutheria; Primates; Catarrhini; Hominoidea; Homo.				
EN	[1]				
RP	SEQUENCE FROM N.A.				
RA	PETERS H.C., KAMMER G., VOLZ A., KAUPMANN K., ZIEGLER A., BETTLER B.,				
RA	EPLEN J.T., SANDER T., RIES O.;				
RT	"Mapping, genomic structure and polymorphisms of the human gababrl				
RT	receptor gene: evaluation of its involvement in idiopathic generalized				
RT	epilepsy."				
RL	Neurogenetics 2:47-54(1998).				
DR	EMBL; AJ010170; CAA09031.1;				

QY 682 ALVIFCSTITLCLVFPVKLITLTNP 709

RESULT 12  
ID Q9W18 PRELIMINARY; PRT; 960 AA.  
AC Q9W18;  
DT 01-NOV-1999 (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
DE 573K1.1.1 (GABA-AMINO BUTYRIC ACID (GABA) B RECEPTOR, 1A).  
GN 573K1.1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA YOUNGER R.;  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AL078630; CAB44990.1;  
KW Receptor.  
SQ SEQUENCE 960 AA; 108216 MW; C07D84FE CRC32;

Query Match 25.6%; Score 1683; DB 11; Length 960;  
Best Local Similarity 36.2%; Pred. No. 0.00e+00;  
Matches 249; Conservative 178; Mismatches 245; Indels 16; Gaps 14;

Db 184 GOACOPAVEMALDVSRRDILPDYELKLIHDSKDCDQATKYLLEYLYNDPIKILMP 243  
QY 31 GRGVLPFAVELAIEQIRNE-SLLRPFLDLRLYTECDNAKGLAFDAIKYGNHLMVFG 89  
Db 244 G-CSSVSTLVAEARMNLIIVLSYSSSPALSNRQFFTFTRHPSATLHNPTRVKLF 302  
QY 90 GVCPSVTIIAESLQGNVLQSLFAATPVADKKKYPFFRVPSDNAVNPAILKLLKH 149  
Db 303 GWKKIATIQOTTEVTSTLDLEERVKAGIEITFRSFDSPAVPVKNLKRQDARIIV 362  
QY 150 YQKRVGLTQDQVRFSEVRNDLTGVLYGEDIEISDTSFSDPCTSVKRLKNDVRIIL 209  
Db 363 GLFYETEARVCEVYKERLFGKYYVFLGWADNWF-KTY-DP-SINCTVEEMTEAVE 419  
QY 210 GOFDQNAKAVFCCAYENMYGSKYQWIIIGWYEPSSWEQVHTSEANSSRCLKNLLA 269  
Db 420 GHITTEIVMLNPANTRSISNMTSQEVVEKITLRLKRHPETGGFQAPLAYDAIWA 479  
QY 270 GYIGVDFEPLSSKOIKTISGKTPQOY-EREYNN-KRSGVGPSKEH-G-YAYDGIWIA 325  
Db 480 LNKTSKG--GGRSGVRLEDNFYNNQITDQIYRAMNSSSFEVSGVGHVFDASGRMA 537  
QY 326 LQAMETLHASSRHQRIDFNFDHTLGRILNANMETNFFGVTVQGVF-RNGERMGTIK 384  
Db 538 IEOLQGSYKKIGYDSTKDDLSW-SKTDKWIIGSPADQTLVITYFRLSKLFISVS 596  
QY 385 FTQFQDSREVYKGEYNADVTLEINDTIRFQSGEPKDKTIILEQLRKISLPLYSIL 444  
Db 597 LSSGLIVLAVVCLSFNIYNSHVRVYIQNSQPNLNNLTAVGCSLALAAVPLGLDGYH 656  
QY 445 LTILGMINASAFLEFNKRNQKLIKMSPPYNNLIILGMLSYASIFLGLDGSFVSE 504  
Db 657 OFPFCVCAWLILGLGFSYGSMTKKIHWVTVFTKKEKWKRLTPKWLATVGLL 716  
QY 505 TETFLCTVRWLTGYTAFGAMFAKTWRVHAIF--KNVRMK-KKIIKDKQLLVIVGGM 561  
Db 717 VGMIDLTALWQIVDPLHRTITETFAKEPKEDIDVLSILPQLEHSSKKMTWLGI 776  
QY 562 LLIDLCILICQWADPLRRTVEKYSMEPPADGDISIRPLEHCENTHTWLGIVAYK 621  
Db 777 GLLLILGIFLAYTKYSYTEKINDHRAVGMATYNNVAVCLITAPVTMLSSQQAFA 836  
QY 622 GLMLFGCFLAWTRNVSIPALNDSKYIGMSVYNGIMCIIGAAVSFTLRDQNPVQ 681  
Db 837 SLAIVFSSYITLVVLPVPMRLITRGE 864

QY 682 ALVIFCSTITLCLVFPVKLITLTNP 709

RESULT 13  
ID C08620 PRELIMINARY; PRT; 960 AA.  
AC C08620;  
DT 01-JUL-1997 (TREMBlrel. 04, Created)  
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)  
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
DE GABA-BRIA OR GABABRI.  
GN GABA-BRIA OR GABABRI.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN-TIF(RAI F [SPF]); TISSUE=CORTEX, AND CEREBELLUM;  
RX MEDLINE: 9722131.  
RA KAUPMANN K., HEGGEL K., HEID J., FLOR P.J., BISCHOFF S., MICKEL S.J.,  
RA MCMASTER G., ANGST C., BITTIGER H., FROESTL W., BETTLER B.;  
RT "Expression cloning of GABA(B) receptors uncovers similarity to  
RT metabotropic glutamate receptors.";  
RL Nature 386:239-246(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA STRAIN-WISTAR;  
RC PFAFF T., MALITSCHKE B., KAUPMANN K., BETTLER B., KARSCHIN K.;  
RT "Alternative splicing generates a novel isoform of the rat  
RT metabotropic GABA(B) receptor.";  
RL Eur. J. Neurosci. 0:0-0(1999).  
DR EMBL: Y10369; CAA71398.1;  
DR EMBL: AF110797; AAD19656.1;  
DR EMBL: AF110796; AAD19656.1; JOINED.  
DR HSSP: P10998; 1VVC.  
DR PFAM: PF00003; 7tm.3; 1.  
DR PFAM: PF01094; ANF\_receptor; 1.  
DR PFAM: PF00084; sushi; 2.  
SQ SEQUENCE 960 AA; 108203 MW; CD3A2D9E CRC32;

Query Match 25.6%; Score 1682; DB 11; Length 960;  
Best Local Similarity 36.2%; Pred. No. 0.00e+00;  
Matches 249; Conservative 178; Mismatches 245; Indels 16; Gaps 14;

Db 184 GOACOPAVEMALDVSRRDILPDYELKLIHDSKDCDQATKYLLEYLYNDPIKILMP 243  
QY 31 GRGVLPFAVELAIEQIRNE-SLLRPFLDLRLYTECDNAKGLAFDAIKYGNHLMVFG 89  
Db 244 G-CSSVSTLVAEARMNLIIVLSYSSSPALSNRQFFTFTRHPSATLHNPTRVKLF 302  
QY 90 GVCPSVTIIAESLQGNVLQSLFAATPVADKKKYPFFRVPSDNAVNPAILKLLKH 149  
Db 303 GWKKIATIQOTTEVTSTLDLEERVKAGIEITFRSFDSPAVPVKNLKRQDARIIV 362  
QY 150 YQKRVGLTQDQVRFSEVRNDLTGVLYGEDIEISDTSFSDPCTSVKRLKNDVRIIL 209  
Db 363 GLFYETEARVCEVYKERLFGKYYVFLGWADNWF-KTY-DP-SINCTVEEMTEAVE 419  
QY 210 GOFDQNAKAVFCCAYENMYGSKYQWIIIGWYEPSSWEQVHTSEANSSRCLKNLLA 269  
Db 420 GHITTEIVMLNPANTRSISNMTSQEVVEKITLRLKRHPETGGFQAPLAYDAIWA 479  
QY 270 GYIGVDFEPLSSKOIKTISGKTPQOY-EREYNN-KRSGVGPSKEH-G-YAYDGIWIA 325  
Db 480 LNKTSKG--GGRSGVRLEDNFYNNQITDQIYRAMNSSSFEVSGVGHVFDASGRMA 537  
QY 326 LQAMETLHASSRHQRIDFNFDHTLGRILNANMETNFFGVTVQGVF-RNGERMGTIK 384  
Db 538 IEOLQGSYKKIGYDSTKDDLSW-SKTDKWIIGSPADQTLVITYFRLSKLFISVS 596  
QY 385 FTQFQDSREVYKGEYNADVTLEINDTIRFQSGEPKDKTIILEQLRKISLPLYSIL 444  
Db 597 LSSGLIVLAVVCLSFNIYNSHVRVYIQNSQPNLNNLTAVGCSLALAAVPLGLDGYH 656

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QY 445 LTIILGIMWASAFLEFNKKNQKLIKMSPPYNNLIILGMLSYASIFLFLDGSFYSEK 504
Db 657 QPFVQCARLWLLGLGSLGYSGMFTKIWMVHTVFTKKEKKEKWKRTLEPKWLYATVGLL 716
QY 505 TFEFLCTVTRWILTVGTYTAFGANFAKTRWRHAIF--KNVNMK-KKIIDOKKLLIVVGGM 561
Db 717 VGMVDLTALAIQVDPVLRHTIETFAKEPKEDIDVSIILPOLHEHCKSKKMTWLGIFYGK 776
QY 562 LLIDLCILICQWADPLRRTRVEKYSMEPDAGRDISIRPLEHCENTHMTWLGIVTAYK 621
Db 777 GLLLLGIFLAYETKSVSTEKINDHRAVGMAYINAVLCLITAPVTMILSSQDAAFAPA 836
QY 622 GLLMFCFLAWETRNVISIPALNDSKYIGSVYNGIMCIIGAASFLTRDQPNVQFCIV 681
Db 837 SLAIVFSSYITLVVLFVFKMRLITRGE 864
QY 682 ALVIFCSTITCLVFPVKLITLRTNPD 709

RESULT 14
ID Q9WU48 PRELIMINARY; PRT; 960 AA.
AC Q9WU48;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DE GABA-B1A RECEPTOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA SULLIVAN R., CHATEAUNEUF A., KOLAKOWSKI L.F. JR., JOHNSON M.P.,
RA BELLEY M., METTERS K., ZAMBONI R., YOUNG R., LIU Q., EVANS J.F.,
RA ABRAMOVITZ M., O'NEILL G.P., NG G.Y.K.
RT "The GABAB receptor heterodimer exhibits guanine nucleotide insensitive
RT high-affinity agonist binding that involves the N-terminal
RT extracellular domain."
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF141168; AAD22194.2; -.
KW Receptor.
SQ SEQUENCE 960 AA; 108274 MW; 7520EB82 CRC32;

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Query Match 25.68; Score 1681; DB 11; Length 960;
Best Local Similarity 36.28; Pred. No. 0.00e+00;
Matches 249; Conservative 177; Mismatches 246; Indels 16; Gaps 14;

Db 184 GOACOPAVEMALEVDVNSRRDILPDYELKLIHDSKCDPGQATKYLYELLYNDPIKILMP 243
QY 31 GRGVLPAVELAIEQIRNE-SLLRPYFLDLRLYDTECDNAKGLKAFYDAIKYGNHLMVFG 89
Db 244 G-CSSVSTLVAEARMNVLVSYGSSSPALSNRQRPFFTHPSATLHNPTRVKLFKEK 302
QY 90 GVCPSVTISIAESLQGNWLVQLSFAATTPVLADKKKYPFFRTVPSDNVAVNPAILKLLKH 149
Db 303 GWKKIATIQOTTEVFTSTLDDLEERVKEAGIETFRQSFSDPAPVVKNLKRODARIIV 362
QY 150 YQMKRVGTLTODVQRFSEVRNDLTGVLYGEDIEISDTSEFSDNPDCTSVKLLKNDVRIL 209
Db 363 GLFYTEARKVCEVYKERLFGKKYVWFLGWYADNWF-KTY-DP-SINCTVEEMTEAVE 419
QY 210 GOFDONMAAKVFCCEAYENMYGSKYQIWIIPGYEPSWQVHEANSRCLKNLLAAME 269
Db 420 GHITTEIVMLNPANTRISNWTQEFVEKLTKLKRHPETGFGFOEAPLAYDAIWALALA 479
QY 270 GYIGVDFEPLSSKOIKITISGKTPOQY-ERYNN-KRSGVGPSEKH-G-YAYDGIWVIATK 325
Db 480 LNKTSKG--GGRSGVRLEDFNYYNQTTIDQIYRAMSSSFEVSGHGVFDASGRMWTLL 537
QY 326 LORAMETLHASSRHQRIOQDFNYTDLTGLRIILNAMNETNFFGVGTGVWF-RNGERMGTIK 384
Db 538 IEOLGGYSKIGYDSTKDDLSW-SKTDKIGGSPADOTLVKTRFSLSKLFISVSV 596

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QY 385 FTQFQDSREVKVGEYNAVADTLEIINDTIRFOGSEPPKDKTIILBOLRKISLPLYSILSA 444
Db 597 LSSIGIVLAVVCLISFNINSHARYIQNSOPNNLNITAVGCSLALAVFPPLGIDGVIHGRS 656
QY 445 LTIILGIMWASAFLEFNKKNQKLIKMSPPYNNLIILGMLSYASIFLFLDGSFYSEK 504
Db 657 QPFVQCARLWLLGLGSLGYSGMFTKIWMVHTVFTKKEKKEKWKRTLEPKWLYATVGLL 716
QY 505 TFEFLCTVTRWILTVGTYTAFGANFAKTRWRHAIF--KNVNMK-KKIIDOKKLLIVVGGM 561
Db 717 VGMVDLTALAIQVDPVLRHTIETFAKEPKEDIDVSIILPOLHEHCKSKKMTWLGIFYGK 776
QY 562 LLIDLCILICQWADPLRRTRVEKYSMEPDAGRDISIRPLEHCENTHMTWLGIVTAYK 621
Db 777 GLLLLGIFLAYETKSVSTEKINDHRAVGMAYINAVLCLITAPVTMILSSQDAAFAPA 836
QY 622 GLLMFCFLAWETRNVISIPALNDSKYIGSVYNGIMCIIGAASFLTRDQPNVQFCIV 681
Db 837 SLAIVFSSYITLVVLFVFKMRLITRGE 864
QY 682 ALVIFCSTITCLVFPVKLITLRTNPD 709

RESULT 15
ID Q9WV16 PRELIMINARY; PRT; 662 AA.
AC Q9WV16;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE 573K1.1.3 (GAMMA-AMINOBUTYRIC ACID (GABA) B RECEPTOR, 1C).
GN 573K1.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA YOUNGER R.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL078630; CAB44992.1; -.
KW Receptor.
SQ SEQUENCE 662 AA; 74593 MW; 3B469368 CRC32;

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Query Match 20.68; Score 1352; DB 11; Length 662;
Best Local Similarity 34.68; Pred. No. 3.12e-255;
Matches 207; Conservative 156; Mismatches 220; Indels 16; Gaps 14;

Db 68 GOACOPAVEMALEVDVNSRRDILPDYELKLIHDSKCDPGQATKYLYELLYNDPIKILMP 127
QY 31 GRGVLPAVELAIEQIRNE-SLLRPYFLDLRLYDTECDNAKGLKAFYDAIKYGNHLMVFG 89
Db 128 G-CSSVSTLVAEARMNVLVSYGSSSPALSNRQRPFFTHPSATLHNPTRVKLFKEK 186
QY 90 GVCPSVTISIAESLQGNWLVQLSFAATTPVLADKKKYPFFRTVPSDNVAVNPAILKLLKH 149
Db 187 GWKKIATIQOTTEVFTSTLDDLEERVKEAGIETFRQSFSDPAPVVKNLKRODARIIV 246
QY 150 YQMKRVGTLTODVQRFSEVRNDLTGVLYGEDIEISDTSEFSDNPDCTSVKLLKNDVRIL 209
Db 247 GLFYTEARKVCEVYKERLFGKKYVWFLGWYADNWF-KTY-DP-SINCTVEEMTEAVE 303
QY 210 GOFDONMAAKVFCCEAYENMYGSKYQIWIIPGYEPSWQVHEANSRCLKNLLAAME 269
Db 304 GHITTEIVMLNPANTRISNWTQEFVEKLTKLKRHPETGFGFOEAPLAYDAIWALALA 363
QY 270 GYIGVDFEPLSSKOIKITISGKTPOQY-ERYNN-KRSGVGPSEKH-G-YAYDGIWVIATK 325
Db 364 LNKTSKG--GGRSGVRLEDFNYYNQTTIDQIYRAMSSSFEVSGHGVFDASGRMWTLL 421
QY 326 LORAMETLHASSRHQRIOQDFNYTDLTGLRIILNAMNETNFFGVGTGVWF-RNGERMGTIK 384
Db 422 IEOLGGYSKIGYDSTKDDLSW-SKTDKIGGSPADOTLVKTRFSLSKLFISVSV 480
QY 385 FTQFQDSREVKVGEYNAVADTLEIINDTIRFOGSEPPKDKTIILBOLRKISLPLYSILSA 444

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Db 481 LSSGLIVAVVCLSFNIYNHVRVYIQNSQPNLNNLTAVGCSLALAAVPLGLDGYHGRS 540
Qy : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
445 LTILGMIWASAFLEFFNIKRNQKLIKMSPPYMNLIILGMLSYASIFLGLDGSFVSEK 504
Db 541 QPPEVCOARLWLLGLGSLGYSMTKIWWVHTVFTKKEKKEWKTLPEPKLYATVGLL 600
Qy : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
505 TFECLCTVRTWILTVGYTTAFGAMFAKTWRVHAIF--KNVRMK-KRIIDOKLLVIVGGM 561
Db 601 VGMDILTLAIWQIVDPLHRTIETFAKEEPKEDIDVSILPQLEHCSSKKMNTWLGLWSF 659
Qy : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
562 LLIDLCILICWQAVDPLRRVTVKYSMEPDPAGRDISIRPLLEHCENTHTIWLGIYVAY 620

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Search completed: Wed Mar 15 21:44:40 2000  
Job time : 1021 secs.



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W A S E L L

(TM)

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MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Wed Mar 15 21:20:43 2000; MasPar time 37.80 Seconds  
Tabular output not generated. 709,480 Million cell updates/sec

Title: >US-09-211-755-2  
Description: (1-898) from US09211755.pep  
Perfect Score: 6573  
Sequence: 1 MPSCPARSATGSLMGLMP.....TASPRHRHVPPSFRVMVSGL 898

Scoring table: PAM 150  
Gap 11

Searched: 82229 seqs, 29864866 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: swiss-prot38  
1:swissprot

Statistics: Mean 56.030; Variance 104.797; scale 0.535

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	241	3.7	908	1	MGR8_MOUSE	1.92e-21
2	236	3.6	871	1	MGR6_RAT	1.52e-20
3	237	3.6	908	1	MGR8_RAT	1.01e-20
4	232	3.5	908	1	MGR8_HUMAN	7.93e-20
5	228	3.5	912	1	MGR4_HUMAN	4.09e-19
6	225	3.4	877	1	MGR6_HUMAN	1.39e-18
7	225	3.4	912	1	MGR4_RAT	1.39e-18
8	214	3.3	912	1	MGR7_RAT	1.19e-16
9	214	3.3	915	1	MGR7_HUMAN	1.19e-16
10	215	3.3	1203	1	MGR5_RAT	7.94e-17
11	215	3.3	1212	1	MGR5_HUMAN	7.94e-17
12	205	3.1	976	1	MGR_DROME	4.26e-15
13	196	3.0	872	1	MGR2_HUMAN	1.45e-13
14	189	2.9	872	1	MGR2_RAT	2.17e-12
15	189	2.9	1079	1	CASR_RAT	2.17e-12
16	187	2.8	877	1	MGR3_HUMAN	4.66e-12
17	187	2.8	879	1	MGR3_RAT	4.66e-12
18	184	2.8	1078	1	CASR_HUMAN	1.46e-11
19	182	2.8	1085	1	CASR_BOVIN	3.11e-11
20	186	2.8	1194	1	MGR1_HUMAN	6.82e-12
21	186	2.8	1199	1	MGR1_RAT	6.82e-12
22	166	2.5	986	1	CYGR_ARBPB	1.17e-08
23	167	2.5	1108	1	CYGR_RAT	8.14e-09

24	159	2.4	1125	1	CYGS_STRPU	SPERACT RECEPTOR PRECU	1.45e-07
25	151	2.3	373	1	BRAC_PSEAE	LEUCINE-, ISOLEUCINE-,	2.40e-06
26	153	2.3	999	1	MGR1_CAEEL	PROBABLE METABOTROPIC	1.20e-06
27	142	2.2	1137	1	CYGL_CAEEL	GUANYLATE CYCLASE RECE	5.16e-05
28	137	2.1	535	1	ANPC_RAT	ATRIAL NATRIURETIC PEP	2.70e-04
29	139	2.1	536	1	ANPC_MOUSE	ATRIAL NATRIURETIC PEP	1.40e-04
30	136	2.1	537	1	ANPC_BOVIN	ATRIAL NATRIURETIC PEP	3.75e-04
31	134	2.0	430	1	YQGE_BACSU	HYPOTHETICAL 48.2 KD P	7.18e-04
32	131	2.0	540	1	ANPC_HUMAN	ATRIAL NATRIURETIC PEP	1.88e-03
33	132	2.0	1103	1	CYGF_BOVIN	RETINAL GUANYLYL CYCLA	1.37e-03
34	134	2.0	1108	1	CYGF_HUMAN	RETINAL GUANYLYL CYCLA	7.18e-04
35	128	1.9	637	1	YHES_ECOLI	HYPOTHETICAL ABC TRANS	4.85e-03
36	127	1.9	938	1	NMZ1_MOUSE	GLUTAMATE [NMDA] RECEP	6.84e-03
37	127	1.9	938	1	NMZ1_HUMAN	GLUTAMATE [NMDA] RECEP	6.84e-03
38	126	1.9	938	1	NMZ1_RAT	GLUTAMATE [NMDA] RECEP	9.06e-03
39	122	1.9	1047	1	ANPB_RAT	ATRIAL NATRIURETIC PEP	3.09e-02
40	126	1.9	1084	1	MYSS_RABIT	MYOSIN HEAVY CHAIN, SK	9.06e-03
41	125	1.9	1937	1	MYSP_HUMAN	MYOSIN HEAVY CHAIN, PE	1.23e-02
42	119	1.8	254	1	YIGE_ECOLI	HYPOTHETICAL 27.9 KD P	7.62e-02
43	117	1.8	488	1	YDP8_SCHPO	HYPOTHETICAL 54.2 KD T	1.38e-01
44	116	1.8	769	1	COMP_BACSU	SENSOR PROTEIN COMP (E	1.84e-01
45	117	1.8	876	1	MYSS_HUMAN	MYOSIN HEAVY CHAIN, SK	1.38e-01

ALIGNMENTS

RESULT 1

ID MGR8\_MOUSE STANDARD; PRT; 908 AA.

AC P47743.

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE METABOTROPIC GLUTAMATE RECEPTOR 8 PRECURSOR.

GN GRM8 OR MGLUR8.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=RETINA;

RX MEDLINE; 95239344.

RA DUVOISIN R.M., ZHANG C., RAMONELL K.;

RT "A novel metabotropic glutamate receptor expressed in the retina and olfactory bulb."

RT J. Neurosci. 15:3075-3083(1995).

RL

CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE ACTIVITY.

CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -!- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN OLFACTORY BULB, ACCESSORY OLFACTORY BULB, AND MAMMARY BODY. WEAKER EXPRESSION IN THE RETINA, AND IN SCATTERED CELLS IN THE CORTEX AND HINDBRAIN.

CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.

CC

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CC

DR EMBL; U17252; AAA68149.1; -.

DR GCRDB; GCR\_1712; -.

DR MGD; MGI:109600; GRM8.

DR PROSITE; PS00979; G-PROTEIN\_RECEP\_F3\_1; 1.

DR PROSITE; PS00980; G-PROTEIN\_RECEP\_F3\_2; 1.

DR PROSITE; PS00981; G-PROTEIN\_RECEP\_F3\_3; 1.

DR PFAM; PF00003; 7tm\_3; 1.

DR PFAM; PF01094; ANP\_receptor; 1.

DR G-protein coupled receptor; 1.

KW Multigene family; 1.17e-08

FT SIGNAL 1 33 POTENTIAL.

FT	CHAIN	34	908	METABOTROPIC GLUTAMATE RECEPTOR 8.
FT	DOMAIN	34	583	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	584	608	I (POTENTIAL).
FT	DOMAIN	609	620	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	621	641	II (POTENTIAL).
FT	DOMAIN	642	647	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	648	668	III (POTENTIAL).
FT	DOMAIN	669	695	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	696	716	IV (POTENTIAL).
FT	DOMAIN	717	746	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	747	768	V (POTENTIAL).
FT	DOMAIN	769	781	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	782	803	VI (POTENTIAL).
FT	DOMAIN	804	818	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	819	843	VII (POTENTIAL).
FT	DOMAIN	844	908	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	95	95	POTENTIAL.
FT	CARBOHYD	298	298	POTENTIAL.
FT	CARBOHYD	452	452	POTENTIAL.
FT	CARBOHYD	480	480	POTENTIAL.
FT	CARBOHYD	565	565	POTENTIAL.
SQ	SEQUENCE	908 AA;	101413 MW;	255B10FF CRC32;
Query Match 3.7%; Score 241; DB 1; Length 908;				
Best Local Similarity 22.1%; Pred. No. 1.92e-21;				
Matches 64; Conservative 99; Mismatches 101; Indels 25; Gaps 22;				
Db	584	AVPVLIILGII-ATTFVIVTFVRYNDPIVRASGRELVSLLTGIFLCYSITFLM-I- 640		
QY	440	SILSAL-TILGIMASAFLEFN-INKRNOKLIKSSPYMNNLIILGMLSVASIFLFGLD 497		
Db	641	AA--PD-TI--ICSFRRIFLGLMCFYSYALLTKTNRIHFIPQGGKSVTAPKFIQSPASQ 695		
QY	498	GSFVSEKTFELCTVTRWLTGVTYTAFAGMFAKTRVHAIFKRVKM-K--KIIRDQKL 554		
Db	696	LVITFSLISVOLGVEVVFVVDPE-PHTIIDYG-BORTLDE-NARGVLK-CDISDLSL-I 750		
QY	555	LVIVGMLLIDLCILICQAVDPLRIVKEYSMEPDAGRDISIRPLEHCENHTMTIWL 614		
Db	751	CSL-GYSILLMW-TC-TVYAIKTRGVPTFNEAKPIGFTMYTTCIIWLAFIPFFGTAQS 807		
QY	615	GIVYAYKGLMLFCFLAWETRNVSIP-ALNDSKYIGSVYVNGIMCIIGAASVFLTRDQ 673		
Db	808	AEKMYIQTTITVSMLSASVSLGMLYMPKYIIFHPQNVQKRSF 856		
QY	674	PNVQFC-IVALVI-I-FCSTITCLVFVPLKITLTNPDAATONRRFQF 719		
RESULT 2				
ID	MGR6_RAT	STANDARD;	PRT;	871 AA.
AC	P35349;			
DT	01-JUN-1994	(Rel. 29, Created)		
DT	01-JUN-1994	(Rel. 29, Last sequence update)		
DT	15-JUL-1999	(Rel. 38, Last annotation update)		
DE	METABOTROPIC GLUTAMATE RECEPTOR 6 PRECURSOR.			
GN	GRW6 OR MGLUR6.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=RETINA;			
RX	MEDLINE; 93280152.			
RA	NAKAJIMA Y., IWAKABE H., AKAZAWA C., NAWA H., SHIGEMOTO R.,			
RA	NAKANISHI S.;			
RT	"Molecular characterization of a novel retinal metabotropic glutamate			
RT	receptor mGluR6 with a high agonist selectivity for L-2-amino-4-			
RT	phosphonobutyrate.";			
RL	J. Biol. Chem. 268:11868-11873(1993).			
CC	-I- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR			
CC	IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE			
CC	ACTIVITY.			
CC	-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			

CC	-I- TISSUE SPECIFICITY: RESTRICTEDLY EXPRESSED IN THE INNER NUCLEAR			
CC	LAYER OF THE RETINA.			
CC	-I- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.			
CC	STRONGEST, TO MGLUR4.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
EMBL;	D13963; BAA03066.1; -			
PIR;	A46742; A46742.			
DR	GCRDB; GCR_0623; -			
DR	PROSITE; PS00979; G_PROTEIN_RECP_F3_1; 1.			
DR	PROSITE; PS00980; G_PROTEIN_RECP_F3_2; 1.			
DR	PROSITE; PS00981; G_PROTEIN_RECP_F3_3; 1.			
DR	PFAM; PF00003; 7tm_3; 1.			
DR	PFAM; PF01094; ANF_receptor; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;			
KW	Multigene family; Vision.			
FT	SIGNAL	1	18	POTENTIAL.
FT	CHAIN	19	871	METABOTROPIC GLUTAMATE RECEPTOR 6.
FT	DOMAIN	19	579	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	580	602	I (POTENTIAL).
FT	DOMAIN	603	616	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	617	637	II (POTENTIAL).
FT	DOMAIN	638	648	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	649	667	III (POTENTIAL).
FT	DOMAIN	668	691	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	692	712	IV (POTENTIAL).
FT	DOMAIN	713	742	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	743	764	V (POTENTIAL).
FT	DOMAIN	765	777	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	778	800	VI (POTENTIAL).
FT	DOMAIN	801	813	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	814	839	VII (POTENTIAL).
FT	DOMAIN	840	871	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	290	290	POTENTIAL.
FT	CARBOHYD	445	445	POTENTIAL.
FT	CARBOHYD	473	473	POTENTIAL.
FT	CARBOHYD	561	561	POTENTIAL.
SQ	SEQUENCE	871 AA;	95089 MW;	81A229E4 CRC32;
Query Match 3.6%; Score 236; DB 1; Length 871;				
Best Local Similarity 22.9%; Pred. No. 1.52e-20;				
Matches 64; Conservative 90; Mismatches 102; Indels 24; Gaps 21;				
Db	586	LAVLG-IMATTIMATFMRHNDPIVRASGRELVSLLTGIFLIYA-I-TF-L---MVAE 638		
QY	445	LTLGIMASAFLEFNINRQK-LIKSSPYMNNLIILGMLSVASIFLGLGDSFVSE 503		
Db	639	PC-AAICAAARLLGLGTLTSYALLTKTNRIYRIFEGOKRSVTPPFISPTSLVITFG 697		
QY	504	KTFELCTVTRWLTGVTYTAFAGMFAKTRVHAIFKRVK--MKKK-IKDQKLLVIVGG 560		
Db	698	LTSLOVGVIAWLGAOPPHSVID-YE-BQRTVDPEQA-RGVLK-CDMSDLSL-IGCL-GY 751		
QY	561	MLLIDLCILICQAVDPLRIVKEYSMEPDAGRDISRPLEHCENHTMTIWIIVYAY 620		
Db	752	SLLLMVTC-TVYAIKARGVPETFEAKPIGFTMYTTCIIWLAFVPIFFGTAQSAEKIYI 809		
QY	621	KGLMLFCFLAWETRNVSIP-ALNDSKYIGSVYVNGIMCIIGAASVFLTRDQPNVQFC 679		
Db	810	QTTITVLSLSASVSLGMLYVPKTYVILFHPQNVQKRRK 849		
QY	680	-IVALVI-I-FCSTITLCLVFVPKLITLTNPDAATONRR 716		
RESULT	3		STANDARD;	PRT;
ID	MGR8_RAT			908 AA.

AC P70579;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE METABOTROPIC GLUTAMATE RECEPTOR 8 PRECURSOR.  
 GN GRM8 OR MGLUR8.  
 OS Rattus norvegicus (Rat).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 97168760.  
 RA SAUGSTAD J.A., KINZIE J.M., SHINOHARA M.M., SEGERSON T.P.,  
 RA WESTBROOK G.L.;  
 RT "cloning and expression of rat metabotropic glutamate receptor 8  
 RT reveals a distinct pharmacological profile";  
 RL Mol. Pharmacol. 51:119-125(1997).  
 CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR  
 CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE  
 CC ACTIVITY.  
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -!- TISSUE SPECIFICITY: PROMINENT EXPRESSION IN OLFACTORY BULB,  
 CC PONTINE GRAY, LATERAL RETICULAR NUCLEUS OF THE THALAMUS, AND  
 CC PIRIFORM CORTEX. LESS ABUNDANT EXPRESSION INCEREBRAL CORTEX,  
 CC HIPPOCAMPUS, CEREBELLUM, AND MAMMILLARY BODY.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC -----  
 CC EMBL; U63288; AAB09537.1; -;  
 DR GCRDB; GCR\_1411; -;  
 DR PROSITE; PS00979; G\_PROTEIN\_RECEP\_F3\_1; 1.  
 DR PROSITE; PS00980; G\_PROTEIN\_RECEP\_F3\_2; 1.  
 DR PROSITE; PS00981; G\_PROTEIN\_RECEP\_F3\_3; 1.  
 DR PFAM; PF00003; 7tm3; 1.  
 DR PFAM; PF01094; ANF\_receptor; 1.  
 DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
 KW Multigene family; Olfaction.  
 FT SIGNAL 1 33 POTENTIAL.  
 FT CHAIN 34 908 METABOTROPIC GLUTAMATE RECEPTOR 8.  
 FT DOMAIN 34 583 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 584 608 I (POTENTIAL).  
 FT DOMAIN 609 620 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 621 641 II (POTENTIAL).  
 FT DOMAIN 642 647 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 648 668 III (POTENTIAL).  
 FT DOMAIN 669 695 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 696 716 IV (POTENTIAL).  
 FT DOMAIN 717 746 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 747 768 V (POTENTIAL).  
 FT DOMAIN 769 781 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 782 803 VI (POTENTIAL).  
 FT DOMAIN 804 818 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 819 843 VII (POTENTIAL).  
 FT DOMAIN 844 908 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 95 95 POTENTIAL.  
 FT CARBOHYD 298 298 POTENTIAL.  
 FT CARBOHYD 452 452 POTENTIAL.  
 FT CARBOHYD 480 480 POTENTIAL.  
 FT CARBOHYD 565 565 POTENTIAL.  
 SQ SEQUENCE 908 AA; 101866 MW; 5043FF81 CRC32;  
 Query Match 32.6%; Score 237; DB 1; Length 908;  
 Best Local Similarity 22.3%; Pred No. 1,01e-20;  
 Matches 63; Conservative 96; Mismatches 100; Indels 24; Gaps 21;

DB 590 IAILGII-ATTFTVIVFVRYNDTPIVRASGRELSYLLTGIFLCYSITFLM-I-AA--PD 644

OY 445 LTILGIMASAFLEFN-IKNRNOKLIKMSPPYMNLIILGMLSYASIFLFGDGSFVSE 503  
 DB 645 -TI--ICSFRIIFLGLMCFSYAALLTKTNRHRIIFEQGKSKVTAPKEIFSPASOLVITES 701  
 OY 504 KFTETCLCTRTWILTGTGTTAFGANFAKTRWRVHAIFKNVNMK-K--KIIKDQKLLVIVGG 560  
 DB 702 LISVQLLGVFVFWVDP-PHTIDYG-EQRTLDPE-NARGVLK-CDISL-ICSL-GY 755  
 OY 561 MLLIDLCLICQAVDPLRRIVKYSMEPPAGRDPSIRPLEHCENTHMTIWLGIYVAY 620  
 DB 756 SILLMV-TC-TVYAIKTRGVPEFNEAKPGFTWTTCTIILWAFIPFPGTAQAEMKI 813  
 OY 621 KGLLMFGCFLAWETRNVSIP-ALNDSKYIGMSVYNGVIMCIIGAAVSFLTRQPNVOFC 679  
 DB 814 QTTTLTVSMISLASVSLGMLYMPKVYIIIFHPEQNVOKRKRSF 856  
 OY 680 -IVALVI-I-FCSITILCLVFPVKLITLIRNPDAATONRRFOF 719  
 RESULT 4  
 ID MGR8\_HUMAN STANDARD; PRT; 908 AA.  
 AC O00222; O15493;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-DEC-1999 (Rel. 39, Last annotation update)  
 DE METABOTROPIC GLUTAMATE RECEPTOR 8 PRECURSOR.  
 GN GRM8 OR MGLUR8.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 98141892.  
 RA WU S., WRIGHT R.A., ROCKEY P.K., BURGETT S.G., ARNOLD J.S.,  
 RA ROSTECK P.R. JR., JOHNSON B.G., SCHOEPP D.D., BELAGAJE R.M.;  
 RT "Group III human metabotropic glutamate receptors 4, 7 and 8:  
 RT molecular cloning, functional expression, and comparison of  
 RT pharmacological properties in RGT cells";  
 RL Brain Res. Mol. Brain Res. 53:88-97(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 97446143.  
 RA SCHERER S.W., SODER S., DUVOISIN R.M., HUIZENGA J.J., TSUI L.C.;  
 RT "The human metabotropic glutamate receptor 8 (GRM8) gene: a  
 RT disproportionately large gene located at 7q31.3-q32.1";  
 RL Genomics 44:232-236(1997).  
 CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR  
 CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE  
 CC ACTIVITY.  
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC -----  
 CC EMBL; U92459; AAB51764.1; -;  
 DR EMBL; U95025; AAB72040.1; -;  
 DR GCRDB; GCR\_1889; -;  
 DR GCRDB; GCR\_2604; -;  
 DR MIM; 601116; -;  
 DR PROSITE; PS00979; G\_PROTEIN\_RECEP\_F3\_1; 1.  
 DR PROSITE; PS00980; G\_PROTEIN\_RECEP\_F3\_2; 1.  
 DR PROSITE; PS00981; G\_PROTEIN\_RECEP\_F3\_3; 1.  
 DR PFAM; PF00003; 7tm3; 1.  
 DR PFAM; PF01094; ANF\_receptor; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
 Multigene family; Olfaction.

```
FT SIGNAL 1 33 POTENTIAL.
FT CHAIN 34 908 METABOTROPIC GLUTAMATE RECEPTOR 8.
FT DOMAIN 34 533 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 584 608 I (POTENTIAL).
FT DOMAIN 609 620 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 621 641 II (POTENTIAL).
FT DOMAIN 642 647 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 648 668 III (POTENTIAL).
FT DOMAIN 669 695 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 696 716 IV (POTENTIAL).
FT DOMAIN 717 746 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 747 768 V (POTENTIAL).
FT DOMAIN 769 781 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 782 803 VI (POTENTIAL).
FT DOMAIN 804 818 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 819 843 VII (POTENTIAL).
FT DOMAIN 844 908 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 95 95 POTENTIAL.
FT CARBOHYD 298 298 POTENTIAL.
FT CARBOHYD 452 452 POTENTIAL.
FT CARBOHYD 480 480 POTENTIAL.
FT CARBOHYD 565 565 POTENTIAL.
FT CONFLICT 194 194 R -> A (IN REF. 2).
FT CONFLICT 460 460 T -> I (IN REF. 2).
FT CONFLICT 642 642 A -> G (IN REF. 2).
FT CONFLICT 768 768 N -> I (IN REF. 2).
FT CONFLICT 904 904 S -> T (IN REF. 2).
SQ SEQUENCE 908 AA; 101741 MW; 188650F CRC32;

Query Match 3.5%; Score 232; DB 1; Length 908;
Best Local Similarity 23.0%; Pred No. 7.93e-20;
Matches 65; Conservative 96; Mismatches 98; Indels 24; Gaps 21;

Db 590 VAILGII-ATTFVIVTFVRYNDTPIVRASGRLSVLLTGIFLCYSITFLM-I-AA--PD 644
QY 445 LTIILGIMASAFLEN-IKRNKLIKSSPYMNNLIILGMLSYASFLEGLDGSFVSE 503
Db 645 -TI--ICSFRRVFLGLGCMFCYSALLTFTNRIHFEGCKSVTAPKFIASPASOLVTIFS 701
QY 504 KTFETLCIVRTWLTVTGTTAFGAMFAKTWRVHAIFKNVKM-K--KIIDKQLLVIVGG 560
Db 702 LISVOLLGVFVWVDDPHIID-YG-EQRTLDPEKA-RGVLK-CDISDLSL-ICSL-GY 755
QY 561 MLIDILCLICQWADPLRRIVERKYSMEPDAGRDISRPLEHCENHTMTWIGVIYAY 620
Db 756 SILLMV-TCTVYANKTRGVP-ETFEAKPIGFTMYTTCIIWLAFIPFFGTAQSAEKMYI 813
QY 621 KGLLMFGCEL-AWETRVNSIPALNDSKYIGMSVYNGVINCIIIGAAVSFLTRQPNVQFC 679
Db 814 QTTILTVMSSLSASVSLGMLYMPKVYIIIFHPQONVOKRKRKF 856
QY 680 -IVALVI-I-FCSTITLCLVFPVKLIITLRTNPDAATQNRRFQF 719

RESULT 5
ID MGR4_HUMAN STANDARD; PRT; 912 AA.
AC Q14833;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 4 PRECURSOR.
GN GRM4 OR MGLUR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA MAKOFF A., LELCHUK R., OXER M., HARRINGTON K., EMSON P.;
RT "Molecular characterization and localization of human metabotropic
glutamate receptor type 4.";
RL Brain Res. Mol. Brain Res. 37:239-248(1996).
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Query Match

3.5%; Score 228; DB 1; Length 912;

```
RN [2]
RX SEQUENCE FROM N.A.
RX MEDLINE; 98141892.
RA WU S., WRIGHT R.A., ROCKEY P.K., BURGETT S.G., ARNOLD J.S.,
RA ROSTECK P.R. JR., JOHNSON B.G., SCHORPP D.D., BELAGAJE R.M.;
RT "Group III human metabotropic glutamate receptors 4, 7 and 8:
RT molecular cloning, functional expression, and comparison of
RT pharmacological properties in RGT cells.";
RL Brain Res. Mol. Brain Res. 53:88-97(1998).
RN [3]
RP SEQUENCE FROM N.A.
RP TISSUE-BRAIN;
RX MEDLINE; 95342351.
RA FLOR P.J., LUKIC S., RUEGG D., LEONHARDT T., KNOEPFEL T., KUHN R.;
RT "Molecular cloning, functional expression and pharmacological
RT characterization of the human metabotropic glutamate receptor type
RT 4.";
RL Neuropharmacology 34:149-155(1995).
CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN THE CEREBELLUM.
CC EXPRESSED AT LOW LEVELS IN HIPPOCAMPUS, HYPOTHALAMUS AND
CC THALAMUS. NO EXPRESSION DETECTED IN LIVER.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR6.
CC -----
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```

```
DR EMBL; X80818; CAA56784.1; -.
DR EMBL; U92457; AAB51762.1; -.
DR GCRDB; GCR_1891; -.
DR GCRDB; GCR_2069; -.
DR MIM; 604100; -.
DR PROSITE; PS00979; G_PROTEIN_RECF_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECF_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECF_F3_3; 1.
DR PFAM; PF00003; 7tm_3; 1.
DR PFAM; PF01094; ANF_receptor; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family.
FT SIGNAL 1 32
FT CHAIN 33 912 METABOTROPIC GLUTAMATE RECEPTOR 4.
FT DOMAIN 33 587 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 588 610 I (POTENTIAL).
FT DOMAIN 611 624 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 625 645 II (POTENTIAL).
FT DOMAIN 646 656 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 657 675 III (POTENTIAL).
FT DOMAIN 676 699 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 700 720 IV (POTENTIAL).
FT DOMAIN 721 750 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 751 772 V (POTENTIAL).
FT DOMAIN 773 785 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 786 808 VI (POTENTIAL).
FT DOMAIN 809 821 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 822 847 VII (POTENTIAL).
FT DOMAIN 848 912 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 98 98 POTENTIAL.
FT CARBOHYD 301 301 POTENTIAL.
FT CARBOHYD 454 454 POTENTIAL.
FT CARBOHYD 484 484 POTENTIAL.
FT CARBOHYD 569 569 POTENTIAL.
SQ SEQUENCE 912 AA; 101867 MW; 740D9054 CRC32;
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Best Local Similarity 21.6%; Pred. No. 4.09e-19;
Matches 62; Conservative 98; Mismatches 100; Indels 27; Gaps 22;

Db 588 AVLPLFLAVVG-IAATLEWITFYRYNDPIIVKASGRELSSVLLAGIFLCYATTEL--M- 643
      :::: |::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 440 SILSA-LTILGNIMASAFLEN-INKRNQKLIKMSPPYNNLIIILGMLSYASIFLGLD 497
      :::: |::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 644 ---IAEPDLGT-CSLRRIFLGLGMSISYAALLTKNRIYRIFEOGKRSVSAPRISASQ 699
      :::: |::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 498 GSFSEKFTETLCTVRTWLTAVGTAFGAMFAKTRVHAIFKNVK--MKK-KIKDQKL 554
      :::: |::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 700 LAIFSLLSLQL-LGICWFWVDSSHVVD-FQQRILDPD-FA-RGVLK-CDISDSL- 753
      :::: |::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 555 LVIVGGMLLIDLCILC-WQAVDPLRRRTVEKYSMEPPDAGRDISIRPLEHCENTHTMIW 613
      :::: |::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 754 ICLL-GYSMLMW-TC-TVYAIKRGVPEFNEAKPIGFTMYTCIIVLAFIPPIFFGTQ 810
      :::: |::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 614 LGIVVAYKGLMLFCFLAWETRNVSIP-ALNDSKYIGMSVYNGIMCIIGAASVFLTRD 672

Db 811 SADKLIYIOTTLTVSVLSUSASVGLMYPKVIYILFHPQONVPRK 857
      :::: |::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 673 OPNVQFC-IVALVI-I-FCSTITLCIVFVKLITLRTNPDAATQNR 716

RESULT 6
ID MGR6_HUMAN STANDARD; PRT; 877 AA.
AC O15303;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 6 PRECURSOR.
GN GRM6 OR MGLUR6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
RP SEQUENCE FROM N.A.
RX HADSHIMOTO T., INAZAWA J., OKAMOTO N., TAGAWA Y., BESSHO Y., HONDA Y.,
RA MASHIME; 97358610.
RA NAKANISHI S.;
RT "The whole nucleotide sequence and chromosomal localization of the
RT gene for human metabotropic glutamate receptor subtype 6."
RL Eur. J. Neurosci. 9:1226-1235(1997).
CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR4.
-----
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DR EMBL: U82083; AAB82068.1; -.
DR GCRDB: GCR_2607; -.
DR MIM: 604096; -.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PFAM; PF00003; 7tm_3; 1.
DR PFAM; PF01094; ANF_receptor; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
Multigene family; Vision.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 877 METABOTROPIC GLUTAMATE RECEPTOR 6.
FT DOMAIN 25 585 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 586 608 I (POTENTIAL).
FT DOMAIN 609 622 CYTOPLASMIC (POTENTIAL).
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TRANSMEM 623 643 II (POTENTIAL).
DOMAIN 644 654 EXTRACELLULAR (POTENTIAL).
TRANSMEM 655 673 III (POTENTIAL).
DOMAIN 674 697 CYTOPLASMIC (POTENTIAL).
TRANSMEM 698 718 IV (POTENTIAL).
DOMAIN 719 748 EXTRACELLULAR (POTENTIAL).
TRANSMEM 749 770 V (POTENTIAL).
DOMAIN 771 783 VI (POTENTIAL).
TRANSMEM 784 806 EXTRACELLULAR (POTENTIAL).
DOMAIN 807 819 VII (POTENTIAL).
TRANSMEM 820 845 CYTOPLASMIC (POTENTIAL).
DOMAIN 846 877 POTENTIAL.
FT CARBOHYD 296 296
FT CARBOHYD 451 451 POTENTIAL.
FT CARBOHYD 479 479 POTENTIAL.
FT CARBOHYD 567 567 POTENTIAL.
SQ SEQUENCE 877 AA; 95436 MW; D5A6C038 CRC32;

Query Match 3.4%; Score 225; DB 1; Length 877;
Best Local Similarity 21.5%; Pred. No. 1.39e-18;
Matches 60; Conservative 91; Mismatches 106; Indels 22; Gaps 19;

Db 592 LAVLGIVATTVVATFVRVYNTPIVRASGRELSSVLLTGIFLIYA-I-TF-L---MVAEP 645
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Qy 445 LTILGNIMASAFLEN-INKRNQKLIKMSPPYNNLIIILGMLSYASIFLGLDGSFVSEK 504
      :::: |::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 646 G-AAVCAARRLFLGLTTLSSALLTKNRIYRIFEOGKRSVTPPPFISPTSQLVTITSL 704
      :::: |::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 505 TFEITCTVTRWLTAVGTAFGAMFAKTRVHAIFKNVK--MKKK-IKDQKLLVIVGGM 561
      :::: |::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 705 TSLQVVGMIANLWLGARPHSVI-D-YE-EQRTVDPEQA-RGVLK-CDMSDSL-IGCL-GY- 757
      :::: |::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 562 LLIDLCILICWQAVDPLRRRTVEKYSMEPPDAGRDISIRPLEHCENTHTMTIWLGIYAYK 621
      :::: |::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 758 SLLLMWTC-TVYAIKARGVPEFNEAKPIGFTMYTCIIVLAFVPIFFGTASAEKIYIQ 816
      |:::|::: |::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 622 GLLMLFCFLAWETRNVSIP-ALNDSKYIGMSVYNGIMCIIGAASVFLTRDQPNVQFC- 679
      :::: |::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 817 TTTLTSLSLASVSGLMYPKVIYILFHPQONVQKRK 855
      |:::|::: |::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 680 IVALVI-I-FCSTITLCIVFVKLITLRTNPDAATQNR 716

RESULT 7
ID MGR4_RAT STANDARD; PRT; 912 AA.
AC P31423;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 4 PRECURSOR.
GN GRM4 OR MGLUR4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE; 92110002.
RA TANABE Y., MASU M., ISHII T., SHIGEMOTO R., NAKANISHI S.;
RT "A family of metabotropic glutamate receptors.";
RL Neuron 8:169-179(1992).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE; 93332699.
RA O'HARA P.J., SHEPPARD P.O., THOGERSEN H., VENEZIA D., HALDEMAN B.A.,
RA MCGRANE V., HOUAMED K.M., THOMSEN C., GILBERT T.L., MULVIHILL E.R.;
RT "The ligand-binding domain in metabotropic glutamate receptors is
RT related to bacterial periplasmic binding proteins.";
RL Neuron 11:41-52(1993).
CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
```





DE METABOTROPIC GLUTAMATE RECEPTOR 5 PRECURSOR.  
GN GRM5 OR MGLUR5.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN;  
RC MEDLINE; 92317054.  
RA ABE T., SUGIHARA H., NAWA H., SHIGEMOTO R., MIZUNO N., NAKANISHI S.;  
RT "Molecular characterization of a novel metabotropic glutamate  
RT receptor mGluR5 coupled to inositol phosphate/Ca2+ signal  
RT transduction.";  
RT J. Biol. Chem. 267:13361-13368(1992).  
RN [2]  
RP SEQUENCE OF 859-923 FROM N.A., AND ALTERNATIVE SPLICING.  
RC TISSUE=BRAIN;  
RC MEDLINE; 93343913.  
RA MINAKAMI R., KATSUKI F., SUGIYAMA H.;  
RT "A variant of metabotropic glutamate receptor subtype 5: an  
RT evolutionally conserved insertion with no termination codon.";  
RL Biochem. Biophys. Res. Commun. 194:622-627(1993).  
CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS  
CC MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-  
CC CALCIUM SECOND MESSENGER SYSTEM AND GENERATES A CALCIUM-ACTIVATED  
CC CHLORIDE CURRENT.  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -!- ALTERNATIVE PRODUCTS: TWO ISOFORMS; 5A (SHOWN HERE) AND 5B; ARE  
CC PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER BY AN INSERTION OF  
CC 32 RESIDUES.  
CC -!- TISSUE SPECIFICITY: WIDELY DISTRIBUTED IN NEURONAL CELLS OF THE  
CC CENTRAL NERVOUS SYSTEM.  
CC -!- MISCELLANEOUS: ACTIVATED BY QUISQUALATE > GLUTAMATE > IBOTENATE >  
CC TRANS-1- AMINOCYCLOPENTYL-1,3-DICARBOXYLATE.  
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.  
CC STRONGEST, TO MGLUR1.  
CC -----  
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CC -----  
DR EMBL; D10891; -; NOT\_ANNOTATED\_CDS.  
DR EMBL; S64315; AAB27666.1; -;  
DR PIR; A42916; A42916.  
DR GCRDB; GCR\_0444; -;  
DR GCRDB; GCR\_0760; -;  
DR PROSITE; PS00979; G\_PROTEIN\_RECEP\_F3\_1; 1.  
DR PROSITE; PS00980; G\_PROTEIN\_RECEP\_F3\_2; 1.  
DR PROSITE; PS00981; G\_PROTEIN\_RECEP\_F3\_3; 1.  
DR PFAM; PF00003; 7tm\_3; 1.  
DR PFAM; PF01094; ANF\_receptor; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
KW Multigene family; Alternative splicing.  
FT SIGNAL 1 20  
FT CHAIN 21 1203 METABOTROPIC GLUTAMATE RECEPTOR 5.  
FT DOMAIN 22 578 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 579 601 I (POTENTIAL).  
FT DOMAIN 602 615 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 616 636 II (POTENTIAL).  
FT DOMAIN 637 647 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 648 666 III (POTENTIAL).  
FT DOMAIN 667 692 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 693 713 IV (POTENTIAL).  
FT DOMAIN 714 736 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 737 758 V (POTENTIAL).  
FT DOMAIN 759 771 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 772 794 VI (POTENTIAL).  
FT DOMAIN 795 800 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 801 826 VII (POTENTIAL).

FT DOMAIN 827 1203 CYTOPLASMIC (POTENTIAL).  
FT CARBOHYD 88 POTENTIAL.  
FT CARBOHYD 209 POTENTIAL.  
FT CARBOHYD 377 POTENTIAL.  
FT CARBOHYD 381 POTENTIAL.  
FT CARBOHYD 444 POTENTIAL.  
FT CARBOHYD 733 POTENTIAL.  
FT VARSPLIC 876 907 MISSING (IN ISOFORM 5A).  
SQ SEQUENCE 1203 AA; 131885 MW; 2955EA33 CRC32;  
Query Match 3.3%; Score 215; DB 1; Length 1203;  
Best Local Similarity 28.3%; Pred. No. 7.94e-17;  
Matches 54; Conservative 57; Mismatches 61; Indels 19; Gaps 17;  
Db 655 AMSYSALVTKTNRIRILAGSK-KKICKTKPRFMSACA-QLVIAF-ILIC---IQ-LGII 707  
QY 522 TTAFGAMFAKTWRVHAIFKNVKKKIIDQKLLVIVGMLLLIDLCILICWQAVDPLRT 581  
Db 708 VALFMEPPDMDHYPISREVLYICNTNLGV-VTPL-GYNGLLIL-SCTFYAFKTRNP 764  
QY 582 VEKYSMEPPDAGRDI-SIRPLLEHCENTHMTITLGIIVYAYKGLLMFGC-FLAWETRNVS 639  
Db 765 -ANFNEAKVIAFTMTTCTIILAFVPI-YFGSNYKIIIMCF-S-VSL-SATVALGCM-FV 818  
QY 640 IPALNDSKTIIGMSVTVNGIMCIIGAASFLTRDQPNVQFCIVALVIFCSTITL-CIIVFV 698  
Db 819 PKVYIILAKPE 829  
QY 699 PKLITLRTNPD 709  
RESULT 11  
ID MGR5\_HUMAN STANDARD; PRT; 1212 AA.  
AC P41594;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-DEC-1999 (Rel. 39, Last annotation update)  
DE METABOTROPIC GLUTAMATE RECEPTOR 5 PRECURSOR.  
GN GRM5 OR MGLUR5.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN;  
RC MEDLINE; 94197696.  
RA MINAKAMI R., KATSUKI F., YAMAMOTO T., NAKAMURA K., SUGIYAMA H.;  
RT "Molecular cloning and the functional expression of two isoforms of  
RT human metabotropic glutamate receptor subtype 5.";  
RL Biochem. Biophys. Res. Commun. 199:1136-1143(1994).  
RN [2]  
RP REVISIONS.  
RA KATSUKI F.;  
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE OF 860-952 FROM N.A.  
RC TISSUE=BRAIN;  
RC MEDLINE; 93343913.  
RA MINAKAMI R., KATSUKI F., SUGIYAMA H.;  
RT "A variant of metabotropic glutamate receptor subtype 5: an  
RT evolutionally conserved insertion with no termination codon.";  
RL Biochem. Biophys. Res. Commun. 194:622-627(1993).  
CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS  
CC MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-  
CC CALCIUM SECOND MESSENGER SYSTEM AND GENERATES A CALCIUM-ACTIVATED  
CC CHLORIDE CURRENT.  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -!- ALTERNATIVE PRODUCTS: TWO ISOFORMS; 5A (SHOWN HERE) AND 5B; ARE  
CC PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER BY AN INSERTION OF  
CC 32 RESIDUES.  
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.  
CC STRONGEST, TO MGLUR1.









Db 185 RTIPNDEHQATAMADIIEYFRNWNVGTIAAD 215  
QY 131 RTVPNDNAVNPAILKLLKHYQWKRYGTLTQD 161

Search completed: Wed Mar 15 21:27:21 2000  
Job time : 398 secs.

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[W][O][R][D] [P][R][O][T][E][I][N] [S][E][Q][U][E][N][C][E] [A][N][A][L][Y][S][I][S]  
\*\*\*\*\*  
(TM)

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MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Wed Mar 15 21:09:20 2000; MasPar time 61.49 Seconds  
688.883 Million cell updates/sec  
Tabular output not generated.

Title: >US-09-211-755-2  
Description: (1-898) from US09211755.pep  
Perfect Score: 6573  
Sequence: 1 MPSCPARSATGPLSLIMGLMP.....TASPRHRHVPPSFRVMVSGL 898

Scoring table: PAM 150  
Gap 11

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: pir62  
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 55.042; Variance 120.918; scale 0.455

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Match	Length	DB ID	Description	Pred. No.	
1	1669	25.4	960	2	JE0356	gamma-aminobutyric ac	4.42e-280
2	241	3.7	908	2	I49142	metabotropic glutamat	6.66e-18
3	236	3.6	871	2	A46742	metabotropic glutamat	3.94e-17
4	225	3.4	912	2	I58149	metabotropic glutamat	1.89e-15
5	225	3.4	912	2	JH0563	metabotropic glutamat	1.89e-15
6	214	3.3	915	2	A49874	metabotropic glutamat	8.61e-14
7	215	3.3	1171	2	A42916	metabotropic glutamat	6.10e-14
8	215	3.3	1180	2	JC2132	metabotropic glutamat	6.10e-14
9	215	3.3	1212	2	JH0561	metabotropic glutamat	6.10e-14
10	189	2.9	872	2	JH0561	metabotropic glutamat	3.96e-10
11	193	2.9	940	2	T02740	hypothetical protein	1.05e-10
12	189	2.9	1079	2	I59362	calcium/polyvalent ca	3.96e-10
13	188	2.9	1218	2	S71376	glutamate receptor ho	5.51e-10
14	187	2.8	879	2	JH0562	metabotropic glutamat	7.66e-10
15	187	2.8	1078	2	S49341	calcium-sensing recep	7.66e-10
16	184	2.8	1078	2	A56715	calcium receptor (clo	2.05e-09
17	182	2.8	1085	2	S40476	Ca(2+)-sensing recept	3.93e-09
18	184	2.8	1088	2	S67115	calcium receptor (clo	2.05e-09
19	186	2.8	1199	2	A41939	G protein-coupled glu	1.06e-09
20	177	2.7	898	2	T05099	hypothetical protein	1.98e-08
21	166	2.5	986	1	OVURGA	speract receptor prec	6.49e-07
22	167	2.5	1108	2	S59915	guanylate cyclase (EC	4.74e-07
23	163	2.5	1525	1	A56699	guanylate cyclase (EC	1.65e-06

24 159 2.4 1125 1 OYURCP speract receptor prec 5.68e-06  
25 152 2.3 373 2 A36125 branched-chain amino 4.76e-05  
26 142 2.2 1005 2 S33525 guanylate cyclase (EC 9.10e-04  
27 137 2.1 535 2 A54155 natriuretic peptide r 3.82e-03  
28 139 2.1 536 2 S71332 natriuretic peptide c 2.16e-03  
29 136 2.1 536 2 A45409 atrial natriuretic pe 5.07e-03  
30 136 2.1 537 1 A28111 natriuretic peptide r 5.07e-03  
31 135 2.1 958 2 T02741 hypothetical protein 6.72e-03  
32 137 2.1 1679 2 T15968 hypothetical protein 3.82e-03  
33 134 2.0 430 2 H69955 conserved hypothetica 8.90e-03  
34 131 2.0 540 1 OYHUCR natriuretic peptide r 2.05e-02  
35 134 2.0 938 2 T01809 hypothetical protein 8.90e-03  
36 132 2.0 1103 2 JC5581 guanylate cyclase (EC 1.55e-02  
37 134 2.0 1108 2 I59385 guanylate cyclase (EC 8.90e-03  
38 128 1.9 637 2 C65129 hypothetical ABC tran 4.67e-02  
39 126 1.9 676 2 S00084 myosin heavy chain, f 8.03e-02  
40 126 1.9 885 2 JN0339 N-methyl-D-aspartate 8.03e-02  
41 126 1.9 901 2 JN0337 N-methyl-D-aspartate 8.03e-02  
42 126 1.9 922 2 JN0338 N-methyl-D-aspartate 8.03e-02  
43 127 1.9 938 2 A46612 N-methyl-D-aspartate 6.13e-02  
44 127 1.9 938 2 S21104 N-methyl-D-aspartate 6.13e-02  
45 126 1.9 938 2 S19710 N-methyl-D-aspartate 8.03e-02

ALIGNMENTS

1 JE0356 #type complete  
gamma-aminobutyric acid receptor B precursor - human  
GABA(B) receptor  
#formal\_name Homo sapiens #common\_name man  
05-Feb-1999 #sequence\_revision 05-Feb-1999 #text\_change  
12-Feb-1999

JE0356  
JE0356  
Grifa, A.; Totaro, A.; Rommens, J.M.; Carella, M.; Roetto,  
A.; Borgato, L.; Zelante, L.; Gasparini, P.  
Biochem. Biophys. Res. Commun. (1998) 250:240-245  
GABA (gamma-amino-butyric acid) neurotransmission:  
Identification and fine mapping of the human GABAB receptor  
gene  
#cross-references MUID:98440782  
#accession JE0356  
#molecule\_type mRNA  
#residues 1-960 #label GRI  
#cross-references GB:Y11044; NID:G2826760  
#note this ORF is not annotated in GenBank entry HSGTHLAL,  
release 109

GENETICS  
#map\_position 6p21.3-6p21.3  
glycoprotein; neurotransmitter receptor; transmembrane  
protein

FEATURE  
1-11 #domain signal sequence #status predicted #label SIG\  
12-960 #product gamma-aminobutyric acid receptor B #status  
predicted #label MAT\  
590-613 #domain transmembrane #status predicted #label TM1\  
627-654 #domain transmembrane #status predicted #label TM2\  
666-687 #domain transmembrane #status predicted #label TM3\  
709-750 #domain transmembrane #status predicted #label TM4\  
767-788 #domain transmembrane #status predicted #label TM5\  
803-825 #domain transmembrane #status predicted #label TM6\  
831-856 #domain transmembrane #status predicted #label TM7\  
23,83,439,481,501, #binding\_site carbohydrate (Asn) (covalent) #status  
513,630 predicted

SUMMARY  
#length 960 #molecular-weight 108148 #checksum 3766  
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Best Local Similarity 36.2%; Pred. No. 4.42e-280;  
Matches 249; Conservative 178; Mismatches 245; Indels 16; Gaps 14;

DB 184 GQACQPAVEALEDVNSRRDILPDYELKLIHHDSKDCPGQATKYLYELLYNDPIKIIMP 243

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QY 31 GGVLPVAVELAEQIRNE-SILRPYFLDLRYDTECDNAKGLKAFYDAIKYGNHLMVFG 89
Db 244 G-CSSVSTLVAEAAWMNLIVLSSGSSPALSNRQRPPTFFTRHPSATLHNPTKVKLFEX 302
QY 90 GVCPSVTSIIAESLOGNLVOLSPAATPVLDKCKYYPFRTVPSDNAVNPAILKLLKH 149
Db 303 KGWKIATIQOTTEVFTSLDDEERKEAGIEITFQSFSDPAVPKMLKQDARIIV 362
QY 150 YCMKRVGTLTDVORFSEVRNLDGLVGEDIEISDESFSNDPCTSVKKLKGNDVRIL 209
Db 363 GLFETEARKVCEVYKERLFGKVVWFLIGVADNNE-KIY-DP-SINCTVDEMTAVE 419
QY 210 GOFDONMAAKVCECAEENMTGSKIWIIPGWIEPWSWEQVHTTANSSRLKNLJAAE 269
Db 420 GHITTEIVMLPANTRSISNNMTSOFVEKLTKRLKRHPETGTFQEAFLAYDAIWLALA 479
QY 270 GYIGVDEPPLSSKOIKTISGTPQOY-EREYNN-KRSGVPSKEH-G-YAIDGIWIAKT 325
Db 480 LNKTSGG--GGRSGVRLEDNFYNNQTTDQIYRAMNSSFEGVSGHVFDASGRMAWTL 537
QY 326 LQRAMETLHASSRHQRIQDFNYDHTLGRILINAMNETNFFGTGQVVF-RNGERMGTIK 384
Db 538 IEQPOGGSYKIGYDPSFKDLSN-SKTDKWIGGSPADOTLVKTRFLSQKLFISVSV 596
QY 385 FTQDSREVKGYNVADTLEIINTIRFQSEPDPKTIIDEQURKISLPLYSILSA 444
Db 597 LSSGLIVLAVVCLSFNYSNVHYIONSQPNLNLTAVGCSLAAAVFPLGLDGYHGRN 656
QY 445 LTILGIMASAFLEFNKRNQKLIKSSPYMNNLIILGMLSVASIFLGLDGSFVSEK 504
Db 657 QPFPVQCARLWLLGLGSLGVSFMFTIWWVHTGFTKKEKWKRTLEPWKLYATVGLL 716
QY 505 TFETLCTVTRTWILVGYTTAFGAMFAKTRWRVHAIF--KNVKMK-KKIIOKQKLLVIVGM 561
Db 717 VGMVDVLTALWQIVDPLHRTTETFAKEPEKEDIDVSLPOLEHCSKRMNTWLGIFYGK 776
QY 562 LLIDLCLICLHCQVADPLRVRVEKYSMEPDAGRDISRPLEHCENHTMTIWIIGVIYAK 621
Db 777 GLLLGLIFLFAKTSYSTEKINDHRVAGMAIYNVAVLCHITAPVTMILSSQDDAAFAFA 836
QY 622 GLMLFGCFLAWETRNVSIPALNSDKYIGMSVYVNGIMCIIGAASVFLTRDQPNVQFCIV 681
Db 837 SLAIVFSSYITLVLPVKMRLLITRGE 864
QY 682 ALVIFCSTITLCLVFPVKLITLTNP 709

RESULT 2
ENTRY 149142 #type complete
TITLE metabotropic glutamate receptor 8 - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
24-Sep-1999
ACCESSIONS I49142
REFERENCE I49142
#authors Duvoisin, R.M.; Zhang, C.; Ramonell, K.
#journal J. Neurosci. (1995) 15:3075-3083
#title A novel metabotropic glutamate receptor expressed in the retina and olfactory bulb.
#cross-references MUID:95239344
#accession I49142
#status preliminary; translated from GB/EMBL/DBDJB
#molecule_type mRNA
#residues 1-908 #label RES
#cross-references EMBL:U17252; NID:9854728; PIDN:AAA68149.1;
PID:9854729

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#gene mGluR8
#classification #superfamily metabotropic glutamate receptor 4
#keywords neurotransmitter receptor
#summary #length 908 #molecular-weight 101413 #checksum 2996
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Query Match 3.7%; Score 241; DB 2; Length 908;
Best Local Similarity 22.1%; Pred. No. 6.66e-18;
Matches 64; Conservative 99; Mismatches 101; Indels 25; Gaps 22;

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QY 440 SILSAL-TILGIMASAFLEFN-IKRNQKLIKSSPYMNNLIILGMLSVASIFLGLD 497
Db 641 AA-PD-TI--ICSPRRIFLGLMCFSYAALLTKTNRHRIFEQKSKSVTAPKFTISPASQ 695
QY 498 GSFVSEKTFEILCTVTRTWILVGYTTAFGAMFAKTRWRVHAIFKNVKMK-K-KIIOKQK 554
Db 696 LVITFSLISVOLLVGVFVWVVDPE-PHTIIDYG-EQRTLDPE-NARGVLK-CDISDLSL-I 750
QY 555 LVIVGMLLIDLCLICLHCQVADPLRVRVEKYSMEPDAGRDISRPLEHCENHTMTIWL 614
Db 751 CSL-CYSILLMV-TC-TVYAIKTRGVPTFNEAKPIGFTMTTTCIWLAFIPFPGTAQS 807
QY 615 GIVYAYKGLMLFGCFLAWETRNVSIP-ALNDSKYIGMSVYVNGIMCIIGAASVFLTRDQ 673
Db 808 ABKMYIQTITLTIVSLSASVSLGMLYMPKYVIIIFHPEQNVQKRKRSF 856
QY 674 PNQVFC-IVALVI-I-FCSTITLCLVFPVKLITLTNPDAATQNRQF 719

RESULT 3
ENTRY A46742 #type complete
TITLE metabotropic glutamate receptor, mGluR6 - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change
24-Sep-1999
ACCESSIONS A46742
REFERENCE A46742
#authors Nakajima, Y.; Iwakabe, H.; Akazawa, C.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi, S.
#journal J. Biol. Chem. (1993) 268:11868-11873
#title Molecular characterization of a novel retinal metabotropic glutamate receptor mGluR6 with a high agonist selectivity for L-2-amino-4-phosphonobutyrate.
#cross-references MUID:93280152
#accession A46742
#status preliminary
#molecule_type nucleic acid
#residues 1-871 #label NAK
#cross-references GB:D13963; NID:g391856; PIDN:BAA03066.1;
PID:d1003572; PID:g391857
#experimental_source retina
#note sequence extracted from NCBI backbone (NCBIN:133246, NCBIP:133250)

CLASSIFICATION #superfamily metabotropic glutamate receptor 4
KEYWORDS G protein-coupled receptor; transmembrane protein
SUMMARY #length 871 #molecular-weight 95088 #checksum 3942

Query Match 3.6%; Score 236; DB 2; Length 871;
Best Local Similarity 22.9%; Pred. No. 3.94e-17;
Matches 64; Conservative 90; Mismatches 102; Indels 24; Gaps 21;

Db 586 LAVLG-IMATTIMATFMRHNDTPIVRASGRSLSVLLTGIFLIYA-I-TF-L---MVAE 638
QY 445 LTILGIMASAFLEFNKRNQK-LIKSSPYMNNLIILGMLSVASIFLGLDGSFVSE 503
Db 639 PC-AAICARLLGLGTTLSYALLTKTNRIYRIFDQGRSVTPPPFISPTSQLVITFG 697
QY 504 KTFETLCTVTRTWILVGYTTAFGAMFAKTRWRVHAIFKNVK--MKKK-IKQDKLLVIVGG 560
Db 698 LTSQVGVGVIANLGAQPHSVID-YE-EQRTVDEQA-RGVLK-CDMSDLSL-IGCL-GY 751
QY 561 MLLIDLCLICLHCQVADPLRVRVEKYSMEPDAGRDISRPLEHCENHTMTIWIIVYAY 620
Db 752 -SLLIMVTC-TVYAIKARGVPETNEAKPIGFTMTTTCIWLAFVPIFFCGTAQSAEKIYI 809
QY 621 KGLMLFGCFLAWETRNVSIP-ALNDSKYIGMSVYVNGIMCIIGAASVFLTRDQPNVQFC 679
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WQREH (TM)

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Mar 15 21:44:59 2000; MasPar time 14.45 Seconds  
Tabular output not generated. 805.278 Million cell updates/sec

Title: >US-09-211-755-2  
Description: (1-898) from US09211755.pep  
Perfect Score: 6573  
Sequence: 1 MPSCPARSATGPLSINGLMP.....TASPRHRHYPPSPRVNVSGL 898

Scoring table: PAM 150  
Gap 11

Searched: 131253 seqs, 12956647 residues

Post-processing: Minimum Match 0\$  
Listing first 45 summaries

Database: a-issued  
1:5A\_COMB 2:5B\_COMB 3:PCT9\_COMB 4:backfiles1

Statistics: Mean 36.509; Variance 186.922; scale 0.195

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	225	3.4	877	2	US-08-407- Sequence 2, Applicatio	1.59e-07
2	225	3.4	912	3	PCT-US91-0 Sequence 19, Applicati	1.59e-07
3	214	3.3	915	1	US-08-453- Sequence 2, Applicati	1.01e-06
4	214	3.3	915	2	US-08-452- Sequence 2, Applicati	1.01e-06
5	214	3.3	915	3	PCT-US94-1 Sequence 2, Applicati	1.01e-06
6	189	2.9	905	1	US-08-072- Sequence 2, Applicati	6.38e-05
7	189	2.9	1079	1	US-08-485- Sequence 8, Applicati	6.38e-05
8	189	2.9	1079	2	US-08-943- Sequence 8, Applicati	6.38e-05
9	189	2.9	1079	1	US-08-484- Sequence 8, Applicati	6.38e-05
10	189	2.9	1079	2	US-08-480- Sequence 8, Applicati	6.38e-05
11	188	2.9	1180	1	US-08-072- Sequence 8, Applicati	7.51e-05
12	188	2.9	1212	1	US-08-072- Sequence 10, Applicati	2.35e-04
13	181	2.8	877	1	US-08-072- Sequence 12, Applicati	2.35e-04
14	187	2.8	879	1	US-08-072- Sequence 6, Applicati	8.85e-05
15	187	2.8	879	1	US-08-486- Sequence 2, Applicati	1.04e-04
16	186	2.8	906	1	US-08-486- Sequence 2, Applicati	1.04e-04
17	186	2.8	906	3	PCT-US91-0 Sequence 17, Applicati	1.04e-04
18	186	2.8	1056	2	US-08-687- Sequence 7, Applicati	1.04e-04
19	186	2.8	1056	2	US-08-687- Sequence 8, Applicati	1.04e-04
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23	184	2.8	1078	2	US-08-480- Sequence 7, Applicati	1.44e-04

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25	182	2.8	1085	2	US-08-480- Sequence 5, Applicatio	2.00e-04
26	182	2.8	1085	1	US-08-484- Sequence 5, Applicatio	2.00e-04
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29	184	2.8	1088	2	US-08-943- Sequence 6, Applicatio	1.44e-04
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31	184	2.8	1088	1	US-08-484- Sequence 6, Applicatio	1.44e-04
32	184	2.8	1088	1	US-08-485- Sequence 6, Applicatio	1.44e-04
33	184	2.8	1180	1	US-08-486- Sequence 8, Applicatio	1.44e-04
34	186	2.8	1199	1	US-08-463- Sequence 2, Applicatio	1.04e-04
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36	186	2.8	1199	2	US-08-465- Sequence 2, Applicatio	1.04e-04
37	186	2.8	1199	1	US-08-455- Sequence 2, Applicatio	1.04e-04
38	186	2.8	1199	3	PCT-US91-0 Sequence 2, Applicatio	1.04e-04
39	184	2.8	1212	1	US-08-486- Sequence 10, Applicati	1.44e-04
40	184	2.8	1219	2	US-08-687- Sequence 6, Applicatio	1.44e-04
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43	127	1.9	922	2	US-08-231- Sequence 14, Applicati	1.11e+00
44	127	1.9	976	2	US-08-231- Sequence 22, Applicati	1.11e+00
45	127	1.9	976	2	US-08-486- Sequence 22, Applicati	1.11e+00

ALIGNMENTS

RESULT 1  
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AC xxxxxx  
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DE Sequence 2, Application US/08407875  
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CC Sequence 2, Application US/08407875  
CC Patent No. 5912122  
CC GENERAL INFORMATION:  
CC APPLICANT: Dagget, Lorrie  
CC APPLICANT: Lu, Chin-Chun  
CC TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTOR  
CC TITLE OF INVENTION: SUBTYPE mGluR6, NUCLEIC ACIDS ENCODING SAME AND USES  
CC TITLE OF INVENTION: THEREOF  
CC NUMBER OF SEQUENCES: 4  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
CC STREET: 444 South Flower Street, Suite 2000  
CC CITY: Los Angeles  
CC STATE: CA  
CC COUNTRY: USA  
CC ZIP: 90071  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC OPERATING SYSTEM: IBM PC compatible  
CC SOFTWARE: PC-DOS/MS-DOS  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/407,875  
CC FILING DATE:  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Reiter, Stephen E.  
CC REGISTRATION NUMBER: 31,192  
CC REFERENCE/DOCKET NUMBER: P41 9921  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 619-546-4737  
CC TELEFAX: 619-546-9392  
CC INFORMATION FOR SEQ ID NO: 2:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 877 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein

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SQ SEQUENCE 877 AA; 95436 MW; 4127619 CN;
Query Match 3.4%; Score 225; DB 2; Length 877;
Best Local Similarity 21.5%; Pred. No. 1.59e-07;
Matches 60; Conservative 91; Mismatches 106; Indels 22; Gaps 19;

Db 592 LAVLGIVATTVAIVFVRYNNTPIVRASGRELSVLLTGIFLIYA-I-TF-L---MVAEP 645
QY 445 LTILGIMASAFLEFNKRNQKLIKMSPPYNNLIILGGLMSYASIFLGLDGSFVSEK 504
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QY 505 TTELTCTVTRWLTITVGYTTAFGAMFAKTRVHAIFKNVK--MKKK-IKKDQKLLVIVGGM 561
Db 705 TSLQVVGMTANLGAAPPISVID-YE-EQRTVDPEQA-RGVLK-CDMSDSL-TGCL-GY- 757
QY 562 LLIDLCILICQAVDPLRRTVEKYSMEPDPAGRDISIRPLEHCENTHMTIWIIGIVAYK 621
Db 758 SLLIMVTC-TVYAIKARGVPETFEAKPIGTMTYTCIIMLAFPIFGTAQSAEKIYIQ 816
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Db 817 TTTLVSLSLASVSGLMIVPKTVIILFHPQNVQKRR 855
QY 680 IVALVI-I-FCSTITICLVFVFKLITLTNPDAATQNR 716

RESULT 2
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Sequence 19, Application PC/TUS9109422
Sequence 19, Application PC/TUS9109422
GENERAL INFORMATION:
CC APPLICANT: Mulvihill, Eileen R.
CC APPLICANT: Hagen, Frederick S.
CC APPLICANT: Houamed, Khaled M.
CC APPLICANT: Almers, Wolfhard
CC TITLE OF INVENTION: G PROTEIN-COUPLED GLUTAMATE RECEPTORS
CC NUMBER OF SEQUENCES: 33
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend
CC STREET: One Market Plaza, Steuart Street Tower
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94103-1492
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US91/09422
CC FILING DATE: 19911212
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/672,007
CC FILING DATE: 18-MAR-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/648,481
CC FILING DATE: 30-JAN-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/626,806
CC FILING DATE: 12-DEC-1990
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Parmelee, Steven W.
CC REGISTRATION NUMBER: 31,990
CC REFERENCE/DOCKET NUMBER: 13952-6PC

TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206) 467-9600
CC TELEFAX: (415) 543-5043
CC INFORMATION FOR SEQ ID NO: 19:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 912 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 912 AA; 102014 MW; 4464621 CN;

Query Match 3.4%; Score 225; DB 3; Length 912;
Best Local Similarity 22.6%; Pred. No. 1.59e-07;
Matches 65; Conservative 93; Mismatches 101; Indels 29; Gaps 23;

Db 598 AVLPLFLAVNG-TAATLFFVVVTVFRNDPIVRASGRELSVYLLAGIFLCYATTEL--M- 643
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Db 700 LAIT--FILISLQLLGICVWVVDPSHVVY-FDQRTLDPR-FA-RGVLK-CDISDSL 753
QY 555 LVIVGGMILLDLCIL-IC-WQAVDPLRRTVEKYSMEPDPAGRDISIRPLEHCENTHMTI 612
Db 754 -ICLL-GYSMLLVY-TG-TVYAIKTRGVPEFNEAKPIGTMTYTCIIVLAFIPIFFGTS 809
QY 613 WLGIVYAYKGLLMLFGCFLANETRNVSIP-ALNDSKYIGMSVYNGIMCIIGAAVSFLTR 671
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QY 672 DQPNVQFC-I VALVI-I-FCSTITICLVFVFKLITLTNPDAATQNR 716

RESULT 3
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AC xxxxxx
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DT
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Sequence 2, Application US/08453862
Sequence 2, Application US/08453862
Patent No. 5738999
GENERAL INFORMATION:
CC APPLICANT: Segerson, Thomas P.
CC APPLICANT: Kinzie, J. Mark
CC APPLICANT: Mulvihill, Eileen R.
CC APPLICANT: Saugstad, Julie A.
CC APPLICANT: Westbrook, Gary L.
CC TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS
CC NUMBER OF SEQUENCES: 5
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend and Crew LLP
CC STREET: Two Embarcadero Center, 8th Floor
CC CITY: San Francisco
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 94111-3834
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/453,862
CC FILING DATE: 30-MAY-1995
CC CLASSIFICATION: 436
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/176,401
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CC FILING DATE: 30-DEC-1993  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Parmelee, Steven W.  
 CC REGISTRATION NUMBER: 31,990  
 CC REFERENCE/DOCKET NUMBER: 13952-18-2  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 206-467-9600  
 CC TELEFAX: 415-576-0300  
 CC INFORMATION FOR SEQ ID NO: 2:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 915 amino acids  
 CC TYPE: amino acid  
 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: protein  
 CC SEQUENCE 915 AA; 102231 MW; 4431664 CN;

Query Match 3.3%; Score 214; DB 1; Length 915;  
 Best Local Similarity 22.9%; Pred. No. 1.01e-06;  
 Matches 65; Conservative 87; Mismatches 106; Indels 26; Gaps 22;

Db 597 LAMLGII-ATIFVMTAFIRYNDTPIVRASGRELVSLLTGIFLCY--IITF-L---MIA- 648  
 QY 445 LITLGMASAFLEFN--IKNRNQLIKMSSPYMNNLIILGGLMSYASIFLFGDGSFVSE 503  
 Db 649 KPDVAVCSFRRVFLGLGMCISYAALLTKNRIYRIFEQGKSVTAPRLISPTSQLAITSS 708  
 QY 504 KTFETLCIVRTWLTIVGYTTAFGAMFAKTRVHAIFKNVEMK-K--KIIDQKLLVIVGG 560  
 Db 709 LISVOLLGVFI-WFGVDPPNIID-YD-EHKTMNPEQA-RGVLK-CDITDLOI-ICSL-G 761  
 QY 561 MLLIDL-CILICQAVDPLRTVEKYSMEPPDAGRDISIRPLEHCENTHMTIWLGIYA 619  
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 QY 620 YKGLLMFCFLAWETRNVSIPA-LNSKYIGMSVYNGVMICIGAAVSEFLTRDQPNVOF 678  
 Db 820 IQTTLTISMNLSASVALGMLYMPKVIYIIIFHPELNVQKRRSF 863

RESULT 4  
 ID US-08-452-734A-2 STANDARD; PRT; 915 AA.  
 XX  
 AC xxxxxx  
 DT  
 DE  
 XX

Sequence 2, Application US/08452734A  
 Sequence 2, Application US/08452734A  
 Patent No. 5831047  
 GENERAL INFORMATION:  
 CC APPLICANT: Segerson, Thomas P.  
 CC APPLICANT: Kinzie, J. Mark  
 CC APPLICANT: Mulvihill, Eileen R.  
 CC APPLICANT: Saugstad, Julie A.  
 CC APPLICANT: Westbrook, Gary L.  
 CC TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS  
 CC NUMBER OF SEQUENCES: 5  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: Townsend and Crew LLP  
 CC STREET: Two Embarcadero Center, 8th Floor  
 CC CITY: San Francisco  
 CC STATE: CA  
 CC COUNTRY: USA  
 CC ZIP: 94111-3834  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: Patentin Release #1.0, Version #1.25  
 CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/452,734A  
 CC FILING DATE: 30-MAY-1995  
 CC CLASSIFICATION: 435  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 08/176,401  
 CC FILING DATE: 30-DEC-1993  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Parmelee, Steven W.  
 CC REGISTRATION NUMBER: 31,990  
 CC REFERENCE/DOCKET NUMBER: 13952-18-1  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 206-467-9600  
 CC TELEFAX: 415-576-0300  
 CC INFORMATION FOR SEQ ID NO: 2:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 915 amino acids  
 CC TYPE: amino acid  
 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: protein  
 CC SEQUENCE 915 AA; 102231 MW; 4431664 CN;

Query Match 3.3%; Score 214; DB 2; Length 915;  
 Best Local Similarity 22.9%; Pred. No. 1.01e-06;  
 Matches 65; Conservative 87; Mismatches 106; Indels 26; Gaps 22;

Db 597 LAMLGII-ATIFVMTAFIRYNDTPIVRASGRELVSLLTGIFLCY--IITF-L---MIA- 648  
 QY 445 LITLGMASAFLEFN--IKNRNQLIKMSSPYMNNLIILGGLMSYASIFLFGDGSFVSE 503  
 Db 649 KPDVAVCSFRRVFLGLGMCISYAALLTKNRIYRIFEQGKSVTAPRLISPTSQLAITSS 708  
 QY 504 KTFETLCIVRTWLTIVGYTTAFGAMFAKTRVHAIFKNVEMK-K--KIIDQKLLVIVGG 560  
 Db 709 LISVOLLGVFI-WFGVDPPNIID-YD-EHKTMNPEQA-RGVLK-CDITDLOI-ICSL-G 761  
 QY 561 MLLIDL-CILICQAVDPLRTVEKYSMEPPDAGRDISIRPLEHCENTHMTIWLGIYA 619  
 Db 762 YSILLMV-TC-TVYAIKTRGVPENFNEAKPIGFTMYTTCIVWLAFIPFGTAQSAEKLY 819  
 QY 620 YKGLLMFCFLAWETRNVSIPA-LNSKYIGMSVYNGVMICIGAAVSEFLTRDQPNVOF 678  
 Db 820 IQTTLTISMNLSASVALGMLYMPKVIYIIIFHPELNVQKRRSF 863  
 QY 679 C-IVALVI-I-FCSTITLCLVFVPLKLTIRTNPDAAATQNRRFQ 719

RESULT 5  
 ID PCT-US94-14989-2 STANDARD; PRT; 915 AA.  
 XX  
 AC xxxxxx  
 DT  
 DE  
 XX

Sequence 2, Application PC/TUS9414989  
 Sequence 2, Application PC/TUS9414989  
 GENERAL INFORMATION:

CC APPLICANT:  
 CC TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS  
 CC NUMBER OF SEQUENCES: 3  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: Patentin Release #1.0, Version #1.25  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: PCT/US94/14989  
 CC FILING DATE:  
 CC CLASSIFICATION:  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 08/176,401  
 CC FILING DATE: 30-DEC-1993  
 CC ATTORNEY/AGENT INFORMATION:

CC NAME: Parmelee, Steven W.  
CC REGISTRATION NUMBER: 31,990  
CC REFERENCE/DOCKET NUMBER: 13952-18PC  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (206) 467-9600  
CC TELEFAX: (415) 543-5043  
CC INFORMATION FOR SEQ ID NO: 2:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 915 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 915 AA; 102231 MW; 4431664 CN;

Query Match 3.3%; Score 214; DB 3; Length 915;  
Best Local Similarity 22.9%; Pred. No. 1.01e-06;

Matches 65; Conservative 87; Mismatches 106; Indels 26; Gaps 22;

Db 597 LAMLGII-ATIFVMTAFIRYNDTPIVRASGRSLSYVLITGIFLCY--LIIF-L---MIA- 648

QY 445 LTILGIMIASAFLEFN-INKRQKLIKMSPPYNNLLIILGGMLSTASIFLFGDGSFVSE 503

Db 649 KPDVAVCSFRRVFLGMLGICISYAALTKTNRIYRIFEQGKKSVTAPRLISPTSLATISS 708

QY 504 KTFETLCTVRLTWTGVYTTAFGAMFAKTWRVHAIFKNVKK-K-KIKDKOKLLVIVGG 560

Db 709 LISVOLLGVFI-WFGVDPPNLIID-YD-EKTMNPEQA-RGVLK-CDITDLOI-ICSL-G 761

QY 561 MLILDL-CILICQVAVDPLRRIVEKISMEPPDAGRIDISIRPLEHCENHTHIIWLGIVYA 619

Db 762 YSILMY-TC-TVYAIKTRGVPEFNKAPIGFTMYTTCIVMLAFIPFIFFGTAQSAEKLY 819

QY 620 YKGLMLFGCLAWETRNVSIPA-LNSDKYIGMSVYVNGIMCIIGAAVSVFLTRDQPNVQF 678

Db 820 IQTTLTISNLSASVALGMLYMPKYIILFHPNLNVOKRSEF 863

QY 679 C-IVALVI-I-FCSTIILCLVFPKLTILRTPDAATQNRFPQF 719

RESULT 6  
ID US-08-072-574-2 STANDARD; PRT; 905 AA.  
XX  
AC xxxxxx  
XX  
DT  
XX

Sequence 2, Application US/08072574

Sequence 2, Application US/08072574  
Patent No. 5521297

GENERAL INFORMATION:

APPLICANT: Daggett, Lorrie  
APPLICANT: Ellis, Steven B.  
APPLICANT: Liaw, Chen

APPLICANT: Pontsler, Aaron

TITLE OF INVENTION: HUMAN MATABOTROPIC GLUTAMATE RECEPTORS,

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark

STREET: 444 South Flower Street, Suite 2000

CITY: Los Angeles

STATE: CA

COUNTRY: USA

ZIP: 00719

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/072,574

FILING DATE: 19930604

CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Reiter, Stephen E.  
CC REGISTRATION NUMBER: 31,192  
CC REFERENCE/DOCKET NUMBER: P41 9383  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 213-622-7700  
CC TELEFAX: 213-489-4210  
CC INFORMATION FOR SEQ ID NO: 2:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 905 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 905 AA; 101396 MW; 4448023 CN;

Query Match 2.9%; Score 189; DB 1; Length 905;  
Best Local Similarity 36.1%; Pred. No. 6.38e-05;

Matches 26; Conservative 22; Mismatches 24; Indels 0; Gaps 0;

Db 159 VIGAGSSVAIQVNLQFLDIPQIAYSATSIDLSKTYKFLRVPSDTLQARMLDI 218

QY 87 VFGVCPSVTSIIAESLQGNLVQLSFAATTPVLADKKKPYFFFTVPSDNAVNPAILKL 146

Db 219 VKRYNWTYVSAY 230

QY 147 LKHYQWKRVTGL 158

RESULT 7

ID US-08-485-588-8 STANDARD; PRT; 1079 AA.  
XX  
AC xxxxxx  
XX  
DT  
XX

Sequence 8, Application US/08485588

Sequence 8, Application US/08485588  
Patent No. 5688938

GENERAL INFORMATION:

APPLICANT: Edward M. Brown

APPLICANT: Steven C. Hebert

APPLICANT: Forrest H. Fuller

APPLICANT: James E. Garrett, Jr.

TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE

TITLE OF INVENTION: MOLECULES

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: First Interstate World Center

STREET: Suite 4700

STREET: 633 West Fifth Street

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: FASTSEQ

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,588

FILING DATE: 7 June, 1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: including application

PRIOR APPLICATION DATA: described below: 9

APPLICATION NUMBER: 08/353,784

FILING DATE: 9 December, 1994

APPLICATION NUMBER: PCT/US/94/12117

FILING DATE: 21 October, 1994





